

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:46:20 ; Search time 39.5 Seconds
(without alignments)
4906.506 Million cell updates/sec

Title: US-09-778-187b-1_COPY_130_1137

Perfect score: 1801

Sequence: 1 atccacacaggtgatgagca.....cgatcacgagcgatgacat 1008

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-O=/cgcn2.1/USPRO.spool/US09778187/runat.20112002.073630.26329/app.query.fasta_1.2318
-DB=PIR_73 -QFMT=fastan -SUFFIX=1pr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.coi -LIST=45
-DOCCALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09778187.ecgn.1.1.113.ecgnat.20112002.073630.26329 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEOUTERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	263.5	14.6	5175	2	T20992	hypothetical prote
2	263.5	14.6	5198	2	T43290	hemiscutin precurs
3	248	13.8	407	2	T08732	hypothetical prote
4	243	13.5	725	2	JEO099	neural cell adhesi
5	239	13.3	1088	1	IXJLNL	neural cell adhesi
6	227	12.6	530	1	A53437	poliovirus recepto
7	227	12.6	4162	2	T42633	connectin/citlin -
8	226	12.5	538	2	T68093	PRR2 delta - human
9	223.5	12.4	7962	2	I38346	elastic titin - hu
10	223	12.4	725	2	JEO100	neural cell adhesi
11	223	12.4	1092	1	JN0635	neural cell adhesi
12	222	12.3	344	2	I56551	neurotrophin - rat
13	222	12.3	467	1	HLMSP3	poliovirus recepto
14	221	12.3	392	2	B44194	poliovirus recepto

15	221	12.3	417	2	A44194	poliovirus recepto
16	219	12.2	518	2	JC4024	poliovirus recepto
17	218.5	12.1	4391	2	A38096	perlecan precursor
18	218	12.1	392	1	RWHUPD	poliovirus recepto
19	218	12.1	417	1	RWHUPA	poliovirus recepto
20	216	12.0	478	1	T53960	PRR2 alpha - human
21	213.5	11.9	812	2	B42632	cell adhesion mole
22	213.5	11.9	932	2	A42632	cell adhesion mole
23	210.5	11.7	345	2	S03199	oploid-binding pr
24	210	11.7	1011	2	T13669	neurotrophin - fr
25	209.5	11.6	584	2	T50419	s-glycerin precurs
26	208.5	11.6	345	2	JC4025	oploid-binding cel
27	206	11.4	702	2	A36319	carcinoembryonic a
28	203.5	11.3	765	2	C42632	cell adhesion mole
29	202.5	11.2	345	2	JC1239	oploid-binding pro
30	202.5	11.2	862	2	I49583	differentiation an
31	202.5	11.2	868	2	A46512	CD22 homolog/8 lym
32	202	11.2	847	2	JH0371	B-cell adhesion pr
33	202	11.2	1443	2	I50600	neogenin - chicken
34	201.5	11.2	338	2	JC1238	oploid-binding pro
35	200	11.1	1323	2	PN0568	connectin 3B - chl
36	197.5	11.0	3707	2	S18252	heparan sulfate pr
37	196.5	10.9	1344	2	T14316	rig-1 protein - mo
38	195.5	10.9	1091	1	ICCHNL	neural cell adhesi
39	195	10.8	588	2	A45254	surface glycoprote
40	195	10.8	1612	2	T30805	ducl1 protein - mo
41	194	10.8	338	2	JC5519	50K glycoprotein p
42	193	10.7	761	1	IJHUNG	neural cell adhesi
43	192.5	10.7	1241	2	T37190	neprin - human
44	191.5	10.6	976	2	T23583	hypothetical prote
45	190	10.5	588	2	JH0506	adhesion molecule

ALIGNMENTS

RESULT 1
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #extL_change 18-Feb-2000
C:Accession: T20992. T24733
R:Stinson, J.
Submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5175 <WIL>
A:Cross-references: EMBL:247068; PIDN:CAAB7335.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone F15G9
R:Kershaw, J.
Submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24733
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5175 <WIL>
A:Cross-references: EMBL:247070; PIDN:CAAB7344.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone T0989
C:Genetics:
A:Gene: CESP:F15G9.4a
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 50

Alignment Scores:
Pred. No.: 2,44e-12
Score: 263.50
Percent Similarity: 43.34%
Best Local Similarity: 24.65%
Query Match: 14.63%
DB: 2
Length: 5175
Matches: 87
Conservative: 66
Mismatch: 129
Indels: 71
Gaps: 15

US-09-778-187B-1_COPY_130_1137 (1-1008) x T20992 (1-5175)

```

QY 40 GTGACAGTATCGAGGAGGAGGTGGCGACCATGCTGCCAAGCATTAAGTAGTACGAC 99
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2200 ValThrAlaIleLysGlyGlyAlaLeuProPheLysCysProIleAsp-----AspSp 2217
QY 100 TCTGTGATTCAGCTACTGAAATCCACAGCAGACCATTTATTTTCAGGAGCTTACGGCT 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2218 Lys-----AsnPhelysGlyGlnIleIleThrLeuArgAsnTyrGlnPro 2232
QY 160 TTG-----AAGGACAGCAGTTTCAGTTGCTGAATTTTCTACGAGTGAACCTC 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2233 IleAspleuGlnAlaGlnAspAlaArgIleThrArgLeu-----SerAsnAspArg 2249
QY 208 AAGATTCATTCAGCAAGCTCTCAATTCATTCAGAGAAAGATCTTTTGGCAGCTCAT 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2250 ArgLeuThrIleLeuAsnValThrGlnAsnAspIleGlnTyrSerCysArgValLys 2289
QY 268 ACCGATCCCCACAGAAAGTTACAC--ACCATCACAGTCTGTCGCCACACGTAAT 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2270 AsnAspAlaGlyGlnAsnSerPheAspPheLysAlaThrValLeuValProProThrIle 2289
QY 325 CTGATGATTCATTCAGCAAGAAC--ACTGCGGTGAGAGGTGAGAGATTGAAGTCAAC 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2290 IleMetLeuAspLysAspLysAsnLysThrAlaValGlnHisSerThrValThrLeuSer 2309
QY 382 TGCATCTCTATGCGCCAGCAGCCAGCAGCATCTACAGTTCAGTTCAGTTCAGGAGG----- 432
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2310 CysProAla---ThrGlyLysProGlnProAspIleThrIlePheLysAspGlyGlnAla 2328
QY 433 -----AACACAGAGCTTAAAGGCAATCGCAG 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2329 IleHisIleGlnAsnIleAlaAspIleIleProAsnGlyGlnLeuAsnGly----- 2345
QY 460 GTGGAAGAGTGTGACAGATGTACATGTGACAGTGTGACAGTGTGACAGTGTGACAG 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2346 -----AsnGlnLeuLysIleThrArgIleLys 2354
QY 520 GAGACAGATGGGGTCCAGTATCTGCGAGTGTGAGCAGCAGCTGGTGGTCAAGAGCTG 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2355 GlnClyAspAlaGlyLysTyrThrCysGlnAlaAspAsnSerAla-----GlySerVal 2372
QY 580 CAGACCCAGCGGTATCTAGAAGTACAGTATTAAGCTTCAAGTGCAC-----ATTGAC 630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2373 GlnGlnAspValAsnValAlaValIleThrIleProLysIleGlnLysAspGlyIlePro 2392
QY 631 ATGACTATCTCTACAGAGCTTAACCCGGAGGAGCGCGCTGTGATTACATGTGAA 690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2393 SerAspTyrGlnSerGln-----GlnAsnGlnArgValAlaIleSerCysPro 2408
QY 691 GCCATCGGAGAGCCCGCTGTGATGTGTAAGTGGTGAAGTGCATGATGAATGACCT 750
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2409 ValThrAlaArgPro---ProAlaLysIleThrIlePheLysAlaGlyLysProLeuGln 2427
QY 751 CAACAGCCGCTACTG-----TGTGGGCCCACTGTTTCATCAATCAACTTAAC 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2428 SerAspLysPheValLysThrSerAlaAsnGlyGlnLysLeuPheLysLeuArg 2447
QY 799 AAAACGATTAATGTCATACCGCTGGAAGCTTCAACATAGTGGGGAAGCTCACTCG 858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2448 GlnThrAspSerSerLysTyrThrCysIleAlaThrAsnGlnAlaGlyLysAspLysArg 2467
QY 859 GATTATTCCTGATGATATACGATCCCGCCACACACTTCCCTCT----- 903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2468 AspPheLysValSerMetLeuValAlaProSerPheAspLysProAsnIleValArg 2487
QY 904 -----CCACAAACACACACACACACACACACACACACACACACACAC 942
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2488 IleThrValAsnSerGlyAsnProSerThrLeuHisCysProAlaLysGlySerProSer 2507
QY 943 ACCATCTTACCATCATCACAGATTCGCCGAGCAGGTGAA 981
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 2508 ProThrIleThrIlePheLysAspGlyAsnAlaIleGln 2520
RESULT 2
T43290
hemiceutinin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence, revision 11-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43290; T20993; T24734
R:Vogel, B.E.; Hedgecock, E.M.
Submitted to the EMBL Data Library, June 1998
A:Description: Hemiceutinin is required for hemidesmosome mediated cell adhesion and ge
A:Reference number: T22396
A:Accession: T43290
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-5198 <VOG>
A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R:Sulston, J.
Submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20993
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F1569.4b
A:Experimental source: clone F1569
R:Kershaw, J.
Submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F1569.4b
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F1569.4b
A:Map position: X
A:Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184
A:2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303
A:4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 51

Alignment Scores:

Pred. No.:	2,44e-12	Length:	5198
Score:	263.50	Matches:	87
Percent Similarity:	43.34%	Conservative:	66
Best Local Similarity:	24.65%	Mismatches:	129
Query Match:	14.63%	Indels:	71
DB:	2	Gaps:	15

US-09-778-187B-1_COPY_130_1137 (1-1008) x T43290 (1-5198)

```

QY 40 GTGACAGTATCGAGGAGGAGGTGGCGACCATGCTGCCAAGCATTAAGTAGTACGAC 99
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2200 ValThrAlaIleLysGlyGlyAlaLeuProPheLysCysProIleAsp-----AspSp 2217
QY 100 TCTGTGATTCAGCTACTGAAATCCACAGCAGACCATTTATTTTCAGGAGCTTACGGCT 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2218 Lys-----AsnPhelysGlyGlnIleIleThrLeuArgAsnTyrGlnPro 2232
QY 160 TTG-----AAGGACAGCAGTTTCAGTTGCTGAATTTTCTACGAGTGAACCTC 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2233 IleAspleuGlnAlaGlnAspAlaArgIleThrArgLeu-----SerAsnAspArg 2249
QY 208 AAGATTCATTCAGCAAGCTCTCAATTCATTCAGAGAAAGATCTTTTGGCAGCTCAT 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2250 ArgLeuThrIleLeuAsnValThrGlnAsnAspIleGlnTyrSerCysArgValLys 2269
QY 268 ACCGATCCCCACAGAAAGTTACAC--ACCATCACAGTCTGTCGCCACACGTAAT 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2270 AsnAspAlaGlyGlnAsnSerPheAspPheLysAlaThrValLeuValProProThrIle 2289
QY 325 CTGATGATTCATTCAGCAAGAAC--ACTGCGGTGAGAGGTGAGAGATTGAAGTCAAC 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:40:00 ; Search time 15.5 Seconds
(without alignments)
5394.599 Million cell updates/sec

Title: US-09-778-187b-1-copy_130_1137

Perfect score: 1801
Sequence: 1 atccccacagtgatgagca.....cgatcagggcagtgatcat 1008

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US09778187/runat.20112002.073629.26309/app_query.fasta_1.2318
-DB=SwissProt_40 -OPMT=fastan -SUFFIX=isp -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNIT=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.coi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NOM=ext -HEADSITE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09778187.ecgn.1.1.45.gunat.20112002.073629.26309 -NCP=6 -ICPU=3
-NO_XPPXY -NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	239	13.3	1088	NCAL_XENLA	P16170 xenopus lae
2	234.5	13.0	515	PVR1_PIG	Q9q176 sus scrofa
3	227.5	12.6	517	PVR1_HUMAN	Q15223 homo sapien
4	227	12.6	530	PVR2_MOUSE	P32507 mus musculu
5	226	12.5	538	PVR2_HUMAN	Q92692 homo sapien
6	223.5	12.4	837	NCM2_MOUSE	Q35136 mus musculu
7	223	12.4	1092	NCM2_XENLA	P36533 xenopus lae
8	222	12.3	344	NTRI_RAT	Q62718 rattus norv
9	221	12.3	417	PVR_CERAE	Q32506 cercopithe
10	219	12.2	337	G55A_CHICK	Q98892 gallus gall
11	218.5	12.1	4393	PGM_HUMAN	P98160 homo sapien
12	217.5	12.0	417	PVR_HUMAN	P13551 homo sapien
13	214.5	11.9	837	NCM2_HUMAN	O15394 homo sapien
14	210.5	11.7	345	OPCM_BOVIN	P11834 bos taurus
15	210	11.7	1242	NPHN_MOUSE	Q9q374 mus musculu
16	208.5	11.6	345	OPCM_HUMAN	O14982 homo sapien
17	208	11.5	515	PVR1_MOUSE	Q931f6 mus musculu
18	208	11.5	1493	NEO1_MOUSE	P97798 mus musculu

19	207.5	11.5	353	1	CEBU_CHICK	Q90773 gallus gall
20	207	11.5	847	1	CD22_HUMAN	P20273 homo sapien
21	206	11.4	702	1	CEA5_HUMAN	P06731 homo sapien
22	203	11.3	1461	1	NEO1_HUMAN	Q92859 homo sapien
23	202.5	11.2	345	1	OPCM_RAT	P32736 rattus norv
24	202.5	11.2	862	1	CD22_MOUSE	P35329 mus musculu
25	202	11.2	1377	1	NEO1_RAT	P97603 rattus norv
26	202	11.2	1443	1	NEO1_CHICK	Q90610 gallus gall
27	197.5	11.0	3707	1	PGM_MOUSE	Q05793 mus musculu
28	195.5	10.9	1091	1	NCAL_CHICK	P13590 gallus gall
29	195.5	10.9	1234	1	NPHN_RAT	Q9r044 rattus norv
30	195	10.8	583	1	C166_MOUSE	Q61490 mus musculu
31	194	10.8	338	1	LAMP_CHICK	Q98919 gallus gall
32	193	10.7	761	1	NCAL_HUMAN	P13592 homo sapien
33	193	10.7	848	1	NCAL_HUMAN	P13591 homo sapien
34	192.5	10.7	1241	1	NPHN_HUMAN	Q06050 homo sapien
35	190	10.5	588	1	C166_CHICK	P42292 gallus gall
36	190	10.5	1447	1	DCC_MOUSE	P70211 mus musculu
37	189.5	10.5	333	1	AMAL_DROME	P15364 drosophila
38	189.5	10.5	646	1	MU18_HUMAN	P43121 homo sapien
39	189	10.5	1036	1	AXO1_CHICK	P28685 gallus gall
40	188.5	10.5	764	1	ICCR_DROME	Q08180 drosophila
41	188	10.4	853	1	NCAL_BOVIN	P31836 bos taurus
42	188	10.4	858	1	NCAL_RAT	P13596 rattus norv
43	187.5	10.4	583	1	C166_HUMAN	Q13740 homo sapien
44	187.5	10.4	873	1	FAST_DROME	P34082 drosophila
45	185.5	10.3	338	1	LAMP_HUMAN	Q13449 homo sapien

ALIGNMENTS

RESULT 1
ID NCAL_XENLA STANDARD; PRT: 1088 AA.
AC P16170:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180).
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90098871; PubMed=2481269;
RA Kriegl P.A., Sakaguchi D.S., Kintner C.R.;
RT "Primary structure and developmental expression of a large
RT cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT molecule (NCAM).";
RL Nucleic Acids Res. 17:10321-10335(1989).
CC -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC NEURITES, ETC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms: N-CAM 180 (shown here) and
CC N-CAM 140: are produced by alternative splicing
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC TISSUE.
CC -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC EARLY NEURAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus.n2p model

Run on: November 20, 2002, 07:46:46 ; Search time 17.5 Seconds
(without alignments)
3389.521 Million cell updates/sec

Title: US-09-778-187b-1_COPY_130_1137
Perfect score: 1801
Sequence: 1 atccacacagctgcatgggca.....cgatcagggcagtgatcat 1008

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+.n2p.model -DEV-xlp
-O-/cg2_1/USPRO.spool/US09778187/runat.20112002_073631_26345/app_query.fasta_1.2318
-DB-Issued_Patents_AA -OPMT-fastan -SUFFIX-ra1 -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdl
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09778187.ecgn1.1.28 @runat.20112002_073631_26345 -ICPU=3
-NO_XMPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cg2_6/ptodata/1/1aa/5a.COMB.pep.*
- 2: /cg2_6/ptodata/1/1aa/5b.COMB.pep.*
- 3: /cg2_6/ptodata/1/1aa/6a.COMB.pep.*
- 4: /cg2_6/ptodata/1/1aa/5b.COMB.pep.*
- 5: /cg2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
- 6: /cg2_6/ptodata/1/1aa/backfile51.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	623.5	34.6	421	2	US-08-660-531-1
3	623.5	34.6	444	4	US-08-659-984A-5
4	623.5	34.6	444	4	US-08-660-531-5
5	232	12.9	393	1	US-08-429-742-2
6	226	12.5	458	4	US-09-435-956A-1
7	206.5	11.5	388	1	US-08-429-742-4
8	206	11.4	642	1	US-08-217-299-1
9	206	11.4	698	2	US-08-602-725-36
10	206	11.4	734	2	US-08-389-459A-17
11	206	11.4	734	2	US-08-987-867A-17
12	194	10.8	1651	4	US-09-540-245A-18

13	193.5	10.7	1395	4	US-09-540-245A-15	Sequence 15, Appl
14	192.5	10.7	1241	4	US-09-040-774-2	Sequence 2, Appl1
15	189	10.5	477	2	US-08-432-016-3	Sequence 2, Appl1
16	189	10.5	477	2	US-08-684-594-3	Sequence 3, Appl1
17	187.5	10.4	583	2	US-08-432-016-2	Sequence 2, Appl1
18	187.5	10.4	583	2	US-08-684-594-2	Sequence 2, Appl1
19	185.5	10.3	308	2	US-08-414-657D-46	Sequence 4, Appl1
20	185.5	10.3	325	2	US-08-414-657D-2	Sequence 2, Appl1
21	185.5	10.3	325	2	US-08-414-657D-41	Sequence 4, Appl1
22	185.5	10.3	325	4	US-09-135-080-2	Sequence 2, Appl1
23	185	10.3	287	2	US-08-414-657D-48	Sequence 4, Appl1
24	185	10.3	304	2	US-08-414-657D-44	Sequence 4, Appl1
25	183.5	10.2	315	2	US-08-414-657D-47	Sequence 4, Appl1
26	183.5	10.2	338	2	US-08-414-657D-42	Sequence 4, Appl1
27	183.5	10.2	338	2	US-08-414-657D-43	Sequence 4, Appl1
28	183.5	10.2	338	4	US-09-135-080-4	Sequence 4, Appl1
29	183	10.2	287	2	US-08-414-657D-49	Sequence 4, Appl1
30	183	10.2	310	2	US-08-414-657D-45	Sequence 4, Appl1
31	180	10.0	1447	4	US-09-041-886-25	Sequence 25, Appl1
32	180	10.0	1447	5	PCT-US94-05277-2	Sequence 2, Appl1
33	179.5	10.0	1297	4	US-09-540-245A-17	Sequence 17, Appl1
34	178	9.9	869	1	US-08-374-834-16	Sequence 16, Appl1
35	178	9.9	869	2	US-08-644-271-29	Sequence 29, Appl1
36	178	9.9	869	4	US-09-077-955-33	Sequence 33, Appl1
37	177.5	9.9	338	2	US-08-414-657D-60	Sequence 60, Appl1
38	177.5	9.9	338	2	US-09-135-080-8	Sequence 8, Appl1
39	176.5	9.8	478	5	PCT-US95-08493-15	Sequence 15, Appl1
40	176.5	9.8	860	5	PCT-US95-08493-19	Sequence 19, Appl1
41	176.5	9.8	868	5	PCT-US95-08493-21	Sequence 21, Appl1
42	175.5	9.7	408	4	US-09-724-864-62	Sequence 62, Appl1
43	174	9.7	607	2	US-08-752-307B-12	Sequence 12, Appl1
44	174	9.7	607	4	US-09-707-802-12	Sequence 12, Appl1
45	174	9.7	607	4	US-09-991-326-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Slnha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 421 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-659-984A-1

Alignment Scores:

Pred. No.:	4,22e-50	Length:	421
Score:	623.50	Matches:	137
Percent Similarity:	57.83%	Conservative:	66
Best Local Similarity:	39.03%	Mismatches:	121
Query Match:	34.62%	Indels:	27
		Gaps:	6

US-09-778-187B-1_COPY_130_1137 (1-1008) x US-08-659-984A-1 (1-421)

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 Db 10 GlycylProleuthrGlnsnValThrValGluGlyThrAlaIleuthr 29
 QY 76 TGCCAAGTCATTAAGAGTACGACTCTGTGATTCAGTCAATCCACAGCGACGC 135
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 Db 30 CysarValaspGlnasnAspAsnThrSerLeuGlnTrpSerProAlaGlnThr 49
 QY 136 ATTTATTTGAGGACTTCAGGCTTTGAGGACAGAGGCTTCAGTTCGATTTTCT 195
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 Db 50 LeuThrPheaspAspLysValLeuThrGlnsnValGluLeuValAlaPhe 69
 QY 196 AGCAGTCAATCAAGATTCATTCAGCAAACTGCTCAATTCGTGATGAAGAATCTT 255
 |||||
 Db 70 TrpIleuSerIleSerValSerAspValSerLeuSerAspGluGlyThr 89
 QY 256 TGCCAGCTCTTACCGATCCCCACAGAAAGTTACACACCATCAGTCTGCTCCCA 315
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 Db 90 CysSerLeuPheThrMetProValLysThrSerLysAlaThrValLeuGlyVal 109
 QY 316 CCACGTATCTGATGATCGATATCCAGAAAGACACTCGCGTGAAGGAGGAGATTGGA 375
 |||||
 Db 110 ProIleuLysProGlnIleSerGlyPheSerSerProValMetGluGlyAspLeuMetGln 129
 QY 376 GTCACTGACCTGCTATGGCCAGCAACCCAGCATATCAGTGGTTCMAAGGAAAC 435
 |||||
 Db 130 LeuThrCysLysThrSerGlySerLysProAlaIleAspIleValGlyThrPheLysAsp 149
 QY 436 ACAGAGCTAAAGCAATCGGAGGTGGAAGTGTCA-----GACATGTACACT 486
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 Db 150 LysGluIleLysAspValLysThrLeuLysGluLysAlaAsnArgLysThrPheThr 169
 QY 487 GTGACAGTCAGTCAAGTGTGAGAGTGCACACAGAGAGCGATGGGTCGCCGATGATGC 546
 |||||
 Db 170 ValSerSerThrLeuAspPheThrValAspArgSerAspGlyValAlaValIleLys 189
 QY 547 CAGGTGAGACCCCTGGGTCACATGGAACCTGCAG---ACCCAGCGATTCAGAGATA 603
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 Db 190 ArgValAspHisGlnSerLeuAsnAlaThrProGlnValAlaMetGlnValLeuGluIle 209
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 |||||
 Db 210 HisThrProSerValLysIle-----IleProSerThrProPheProGlnGlu 226
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 |||||
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 QY 724 TGGGTGAGAGTCATGATGAATG-----CCTCAACAGCGCTACGTCTGGGCCCAAC 777
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 Db 247 TrpThrLysAspGlyGlyLeuProAspProAspArgMetValValSerGlyArgGlu 266
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Db 267 LeuAsnIleLeuPheLeuAsnLysThrAspAsnGlyThrTyArgCysGluAlaIleThrAsn 286
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 Db 287 ThrIleGlyIleSerSerAlaGluThrValLeuIleValHisAspValProAsnThrLeu 306
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 Db 327 ThrThrSerProThrThrSerAlaThrThrSerSerIleArgAspProAsnAlaLeuAla 346
 QY 976 GGTGAGAGAGCTCGATCAGGAGGTGATCAT 1008
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 Db 347 GlycylAsnGlyPro-----AspHis 353

RESULT 2

US-08-660-531-1
 ; Sequence 1, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-660-531-1

Alignment Scores:

Pred. No.:	4,22e-50	Length:	421
Score:	623.50	Matches:	137
Percent Similarity:	57.83%	Conservative:	66
Best Local Similarity:	39.03%	Mismatches:	121
Query Match:	34.62%	Indels:	27
		Gaps:	6

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OM nucleic - protein search, using frame_plus.n2p model

Run on: November 20, 2002, 07:44:26 ; Search time 69.25 Seconds

(Without alignments)
5998.426 Million cell updates/sec

Title: US-09-778-187b-1_COPY_130_1137

Perfect score: 1801

Sequence: 1 atccccacaggtcgtatgagca.....cgatcacggcgatgatcat 1008

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=SPTRMBL_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.col -LIST=45
-DOCALLIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: SPTRMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp_invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organism:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*
15: sp-virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1758	97.6	442	4	Q9BY67	Q9BY67 homo sapien

2	1741	96.7	445	11	Q8RAL1	Q8RAL1 mus musculus
3	1725.5	95.8	456	11	Q8R5M8	Q8R5M8 mus musculus
4	1725.5	95.8	494	11	Q8CRY3	Q8CRY3 mus musculus
5	1529	84.9	336	11	Q9D6E7	Q9D6E7 mus musculus
6	1180	65.5	295	11	Q9J2H8	Q9J2H8 mus musculus
7	1157.5	64.3	306	11	Q8QY14	Q8QY14 mus musculus
8	1137	63.1	295	11	Q9QYL6	Q9QYL6 mus musculus
9	1048	58.2	289	11	Q9QYL5	Q9QYL5 mus musculus
10	1024.5	56.9	278	11	Q9QYL3	Q9QYL3 mus musculus
11	622	34.5	388	11	Q8RA64	Q8RA64 mus musculus
12	609	33.8	381	4	Q9Y4A4	Q9Y4A4 homo sapien
13	482.5	26.8	396	11	Q9N9N28	Q9N9N28 mus musculus
14	469.5	26.1	432	4	Q9UJPL	Q9UJPL homo sapien
15	301	16.7	549	11	Q9D006	Q9D006 mus musculus
16	298	16.5	549	11	Q9JLB9	Q9JLB9 mus musculus
17	292	16.2	549	4	Q9NQS3	Q9NQS3 homo sapien
18	287	15.9	438	11	Q9JLB7	Q9JLB7 mus musculus
19	285	15.8	510	11	Q9JLB8	Q9JLB8 mus musculus
20	263.5	14.6	5198	5	Q76518	Q76518 caenorhabditis
21	255	14.2	1482	5	Q9V4Y0	Q9V4Y0 drosophila
22	250	13.9	439	13	Q57349	Q57349 gallus galli
23	248	13.8	407	4	Q9Y412	Q9Y412 homo sapien
24	243.5	13.5	1102	11	Q9J2H7	Q9J2H7 mus musculus
25	243	13.5	725	13	Q73633	Q73633 xenopus laevis
26	235	13.0	393	4	Q95727	Q95727 homo sapien
27	234.5	13.0	1032	13	Q8UVD6	Q8UVD6 brachydanio
28	227	12.6	4162	13	Q98918	Q98918 gallus galli
29	224.5	12.5	605	4	Q96J84	Q96J84 homo sapien
30	223.5	12.4	7962	4	Q10465	Q10465 homo sapien
31	223.5	12.4	34350	4	Q8WZ42	Q8WZ42 homo sapien
32	223	12.4	725	13	Q73634	Q73634 xenopus laevis
33	222	12.3	467	11	Q91V79	Q91V79 mus musculus
34	222	12.3	1380	4	Q9HCK4	Q9HCK4 homo sapien
35	222	12.3	1675	13	Q98SM4	Q98SM4 brachydanio
36	221.5	12.3	975	5	Q97174	Q97174 drosophila
37	221	12.3	344	11	Q99P10	Q99P10 mus musculus
38	220	12.2	344	4	Q9P121	Q9P121 homo sapien
39	220	12.2	449	4	Q90E16	Q90E16 mus musculus
40	219.5	12.2	1056	13	Q90Z03	Q90Z03 xenopus laevis
41	219	12.2	344	13	Q9DF61	Q9DF61 gallus galli
42	219	12.2	1060	11	Q90Z13	Q90Z13 rattus norvegicus
43	217.5	12.1	959	5	Q9N9Y9	Q9N9Y9 drosophila
44	217.5	12.1	968	5	Q9W4T9	Q9W4T9 drosophila
45	217.5	12.1	4370	4	Q9H3V5	Q9H3V5 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9BY67	PRELIMINARY:	PRT:	442 AA.
AC	Q9BY67;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Nectin-like protein 2.			
GN	NECL2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RA	Zhou Y., Du G., Chen J., Yuan J., Qiang B.;			
RT	"Cloning of a novel human cDNA encoding a member of the Immunoglobulin superfamily."			
RT	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF132811; AAF69029.1; -			
DR	InterPro: IPR003598; Ig.			
DR	InterPro: IPR003598; Ig_C2.			
DR	InterPro: IPR003600; Ig_Like.			
DR	InterPro: IPR003600; Ig_MHC.			
DR	Pfam: PF00047; Ig_3.			

DR SMART: SM00409; IG: 3.
 DR SMART: SM00408; IGC2: 3.
 DR SMART: SM00410; IG_1like: 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Alignment Scores:

Align. No.:	1.96e-146	Length:	442
Score:	1758.00	Matches:	335
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	0
Query Match:	97.61%	Indels:	0
DB:	4	Gaps:	0

US-09-778-187B-1_COPY_130_1137 (1-1008) x Q9BY67 (1-442)

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Db 39 ILeProthrglyaspjglnasnleuphethrlyspvalthrvalilegluglyglu 58
QY 61 GTTGCAGCATCAGTCCCAAGTCATAGAGTACGACTCTGTATCAGTCACTCAAT 120
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Db 59 ValaIarhrliesercysglnvalasnlyseraspserValileglnleuasn 78
QY 121 CCCACAGCAGACCATTTATTTACAGGACTTCAGGCTTTGAAGACAGAGGTTTCAG 180
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Db 79 ProasnarglnthrIletryrPhearqaspPhearqProleuylsaspserArgPhegln 98
QY 181 TTGCTGAATTTTCTACAGTCAAGTCAAGTATCATTCAGCAAGCGTCAATTCTGAT 240
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Db 99 LeuLeuasnheserSerSerSerGlnleuylsValiserleuhrasnvaliserIleSerasp 118
QY 241 GAAGGAAGATACATTTCAGCTCTATACGATCCCGACAGAAAGTTACACCCATC 300
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Db 119 GlUGlyrgrtyrPheCysglnleuYrThrAspProProglinsuYrYrThrIle 138
QY 301 ACAGTCTGTGTCACACACGTAATCTGATGATGATTCAGAAAGACACTGGCGTGAA 360
   |||
Db 139 ThrValleuvalProProaargasnleuMetIleaspIleglinaargaspThrAlaValglu 158
QY 361 GGTGAGAGATTAAGTCAACTGCTATGCGCCAGTGGCCAGACGACGACATCATCAGG 420
   |||
Db 159 GlYgluglnuilegluvalasnCysThrAlaMetAlaSerlyspProalathrThrIlearg 178
QY 421 TGGTTCAAGGGAACACAGAGCTAAAGCAATCGAGGTGGAAGATGGGTCCAGATG 480
   |||
Db 179 TrpPheylsGlnasnThrGlnleuYsGlyLysserGlnuValGlnuIurPserAspMet 198
QY 481 TACAGTGTGACAGTCACTGATGCTGAGGTGACACAGAGACATGGGGTCCAGTG 540
   |||
Db 199 TyrThrValThrIserGlnleuMetleuYsValHisIlysglnaspaspGlyValProval 218
QY 541 ATGTGCGAGGTGAGACACCTGCGGTCTACAGAAACCTGAGACCCGCGGTATCTGAA 600
   |||
Db 219 IleCysglnvalGlnHisProAlaValThrGlyAsnleuGlnThrGlnArgIlyrleGln 238
QY 601 GTACAGTAATAAGCTCAAGTGCACATTCAGATGACTTATCTCTACAAAGCTTAACCCGG 660
   |||
Db 239 ValGlntyrlyspProGlnValHisIleGlnMetThrTyrrProleuGlnGlyleuThrArg 258
QY 661 GAAGGGAGACCGCTGAGTTAACAATGGAAGCCATGGGAAGCCCGACCTGATGAGTA 720
   |||
Db 259 GlUGlyaspIleleuGlnleuThrCysGlnAlaIleGlyLysProGlnProValIleVal 278
QY 721 ACTTGGGTGAGTGCATGATGAATGAGCTCAACACGCGCTACTGCTGGGCCAACCTG 780
   |||
Db 279 ThrTrpValargValaspaspGlnMetProGlnHisAlaValIleuSerGlyProasnleu 298
QY 781 TTCATCAATAACCTAAACAAACAGATATGATGATACCGCTGTGAAGCTTCAACATA 840
   |||
Db 299 PheIleasnlnleuasnlysrThrAspasnGlyThrTyrrgCysglnuAlaSerasnIle 318
QY 841 GTGGGGAAGCTCACTCGGATTTATGCTGTATGTATACGATCCCCCACAACATTCCT 900
   |||

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Db 319 ValIGlysalanHisSerAspTyrMetleuYrValIyAspProProthrThrIlePro 338
QY 901 CCTCCCAACAAACACACACACACACACACACACACACACACACACACACACATC 960
   |||
Db 339 ProProthrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 358
QY 961 ACAGATTCGCCGAGCAGTGAAGAAGCGTGCATCGAGCGAGTGCATCAT 1008
   |||
Db 359 ThrspserargAlaGlyGlnGlnGlySerIleargAlaValaspHis 374

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RESULT 2

Q8R4L1 PRELIMINARY; PRT; 445 AA.
 ID Q8R4L1;
 AC Q8R4L1;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE Tumor suppressor in lung cancer 1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Fukami T., Maruyama T., Murakami Y.;
 RT "Identification of murine orthologue of the TSLC1 gene."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF34663; MIM:67361; -.
 SQ SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;

Alignment Scores:

Align. No.:	6.19e-145	Length:	445
Score:	1741.00 <td>Matches:</td> <td>332</td>	Matches:	332
Percent Similarity:	99.11%	Conservative:	1
Best Local Similarity:	98.81%	Mismatches:	3
Query Match:	96.67%	Indels:	0
DB:	11	Gaps:	0

US-09-778-187B-1_COPY_130_1137 (1-1008) x Q8R4L1 (1-445)

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QY 1 ATCCCCACAGGTGATGGGCGAATCTGTTTACGAACAGCTGACAGTGAAGGAGAG 60
   |||
Db 42 ILeProthrglyaspjglnasnleuphethrlyspvalthrvalilegluglyglu 61
QY 61 GTTGCAGCATCAGTCCCAAGTCATAGAGTACGACTCTGTATCAGTCACTCAAT 120
   |||
Db 62 ValaIarhrliesercysglnvalasnlyseraspserValileglnleuasn 81
QY 121 CCCACAGCAGACCATTTATTTACAGGACTTCAGGCTTTGAAGACAGAGGTTTCAG 180
   |||
Db 82 ProasnarglnthrIletryrPhearqaspPhearqProleuylsaspserArgPhegln 101
QY 181 TTGCTGAATTTTCTACAGTCAAGTCAAGTATCATTCAGCAAGCGTCAATTCTGAT 240
   |||
Db 102 LeuLeuasnheserSerSerSerGlnleuYsValiserleuhrasnvaliserIleSerasp 121
QY 241 GAAGGAAGATACATTTCAGCTCTATACGATCCCGACAGAAAGTTACACCCATC 300
   |||
Db 122 GlUGlyrgrtyrPheCysglnleuYrThrAspProProglinsuYrYrThrIle 141
QY 301 ACAGTCTGTGTCACACACGTAATCTGATGATGATTCAGAAACAGCTGCGGTGAA 360
   |||
Db 142 ThrValleuvalProProaargasnleuMetIleaspIleGlnlyspThrAlaValglu 161
QY 361 GGTGAGAGATTAAGTCAACTGCACTGCTATGCGACAGACGACGACTATCAGG 420
   |||
Db 162 GlYgluglnuilegluvalasnCysThrAlaMetAlaSerlyspProalathrThrIlearg 181
QY 421 TGGTTCAAGGGAACACAGAGCTAAAGCAATCGAGGTGGAAGAGTGTGACATG 480
   |||
Db 182 TrpPheylsGlnasnlysglnleuYsGlyLysserGlnuValGlnuIurPserAspMet 201
   |||

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Oy	481	TACACTGTGACCACTCAGCTGATGCTCTGAAGTGCACAGAGACAGATGGCGCTCCAGTG	540
Db	202	TycthrVal1thrSerGinLeuMetLeuLysVal1His1LysGlnSparSpGlyVal1ProVal	221
Oy	541	ATTCGCCGATGGAGACCCCGCGGTCTACGTGGAAACCTGCGAGACCCGCGGTACTAGAA	600
Db	222	IleCysGlnVal1GlnHisProVal1ThrGlyLysMetGlnThrGlnAryrLysGlu	241
Oy	601	GTACAGTAAAGCCTCAAGTGCACATTCAGATGACTTATGCTCTACAAAGCCTTAACCCGG	660
Db	242	ValGlnTyLysProGlnVal1His1IleGlnMetThrTyLysProLeuGlnGlyLeuThrArg	261
Oy	661	GAAGCGACCGCGCTTGAGTTAACTATGTGAAGCCATCGCGAAAGCCCGCTGTGATGGTA	720
Db	262	GlyGlySparPalapheGlnLeuThrCysGlnVal1IleGlyLysProGlnProVal1MetVal	281
Oy	721	ACTGGCGTACAGTGCATGATGAATAATCCCTCAACACCCCGTACTGTGTGGCCCAACTG	780
Db	282	ThrTrpVal1ArgVal1AspAspGlnMetProGlnHis1Val1LeuSerGlyProAsnLeu	301
Oy	781	TTTCATCAATTAACCTTAACAAACAAAGATATGATACATACCGCTGTGAAAGCTTAACATA	840
Db	302	Phel1AsnAsnLeuAsnLysThrAspAsnGlyThrTyLysArgGlnVal1AsnSerAsnIle	321
Oy	841	GTGGGGAAGGTCTACCTGGATTAATGCTGTATGCTATACATATCCCGCCCAACATATCCCT	900
Db	322	ValGlyLysVal1Asn1SerAspTyLysMetLeuTyVal1TyLysProProThrTrh1IlePro	341
Oy	901	CCTCCACACAAACACACACACACACACACACACACACACACACATCTTACATCATATC	960
Db	342	ProProThrTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrhTrh	361
Oy	961	ACAGATTCCCGACAGCGTGAAGAAAGCTCGATCAAGGCACTGATCAT	1008
Db	362	ThrAspSerArgGalaGlyGlnGlyThrIleGlyVal1Val1AspHis	377
RESULT 3			
Oy	08R5M8	PRELIMINARY:	PRT: 456 AA.
AC	08R5M8:		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	RA175.		
GN	RA175.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.		
OX	NCBI_taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Momoi T.;		
RT	"Biological function of RA175, a new member of immunoglobulin super		
RT	family.";		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB064265; BAB83501.2; -		
SO	SEQUENCE 456 AA; 49787 MW; 3226866A4BC1C7F CRC64;		
Alignment Scores:			
Pred. No.:	1,44e-143	Length:	456
Score:	1725.50	Matches:	332
Percent Similarity:	95.97%	Conservative:	1
Best Local Similarity:	95.68%	Mismatches:	3
Query Match:	95.81%	Indels:	11
DB:	11	Gaps:	1

Qy 1 ATCCCCACAGCTAATGGGAGAAATCTGTTTACGAAAGACGTGACATGTCAGAGGAGAG 60
|||
Db 42 ILleRrothrlYaspGlyGlnmsnleuPheRtrYasPValTrhValILleGluGlyGlu 61

[illegible]

RESULT 4	
09CRV3	
ID 09CRV3	PRELIMINARY;
AC 09CRV3;	PRT; 494 AA
DT 01-JUN-2001 (Tremblay, 17, Created)	

DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE 3100001108RIK protein (Fragment).
GN IGSF4 OR 3100001108RIK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hornann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuke S.,
RA Hayashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013911; BAB29050.1; -.
DR MGD; MG1:1889272; Igsf4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG2; 3.
DR SMART; SM00408; IG2; 3.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 494 AA: 53946 MW: F5E09ABA1857ABCO CRC64;

Alignment Scores:
Pred. No.: 1,47e-143 Length: 494
Score: 1725.50 Matches: 332
Percent Similarity: 95.97% Conservative: 1
Best Local Similarity: 95.68% Mismatches: 3
Query Match: 95.81% Indels: 11
DB: 11 Gaps: 1

US-09-778-187b-1_copy_130_1137 (1-1008) x Q9CRY3 (1-494)
QY 1 ATCCCAAGGTGAGGAGATCTGTTACGAAGAGCTGACAGTGCAGGAG 60
DB 80 ILEPRTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 99
QY 61 GTTGGCAGCATCATGTTGCCAAGTCAATAGAGTGCAGTCTGTGATTCAGTGAAT 120
DB 100 VALAIAATHRIIESERCYSGLINVAIAANLVSERASPSPSERVALILEGILNLEULVASHN 119
QY 121 CCCAAGAGGAGACATTTATTTTCAGGAGCTTACAGCCTTTGAAGAGCAGAGCTTTGAG 180
DB 120 PROASATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 139
QY 181 TTGCTGAATTTTCTAGAGTGAAGTCAAGTATCATTTGACAAACGCTCAATTTTGAT 240
DB 140 LEULEUASHNPHESERISERISERISERISERISERISERISERISERISERISER 159
QY 241 GAAGAAGATACCTTTTCCAGCTCTATACGATCCCAACAGGAAGTTACACCACATC 300

DB 160 GLUULYATGTYRPHCYSGINLEUTYTHRASPRPROGLINGUSERTYTHRTILE 179
QY 301 ACACTCTGCTGCCACACAGTAAATCTGATGATGATTCAGAAAGCACTGGGGTGAA 360
DB 180 THYVALLEUVALPROPPOAAGASINLEMETCLESPILLEINLYSASPTTHALVALGLU 199
QY 361 GGTGAGAGATGTAAGTCAACTGCATGCTATGAGCCAGCAAGCAGCAGCAGTATCAGG 420
DB 200 GLYGLULILEGLIUVAVIANCYSYTHALAMECLASERTYSPROALATHRTTHILEARG 219
QY 421 TGGTTCAAGGAGAACACAGAGCTAAAGGCAAAATCGAGGTGGAAGAGTGTGACAGATG 480
DB 220 TRPHELYSGLYSNLYSGILEULYSGLYLSERSGLIUVAGLUGIUTRPSERASPMET 239
QY 481 TACACTGTGACAGTACGCTGATGCTAAGGTGACACAGAGAGAGAGTGGGCTCCAGTG 540
DB 240 TYTHRYVALTHRSERGLNLEUMETLEULYSVALHISYSGILNPSAPSPGLIYVALPROVAL 259
QY 541 ATCTGCCAGGTGAGACACCTGCGGTCACTGAGAAACCTGCAGACCCAGCGTATCTAGAA 600
DB 260 ILECYSLINVALGUNIHSPPROALAVALTHTGLYASNLEULNTHRGALGYTRLEUGLU 279
QY 601 GTACAGTATAGCTCCTCAAGTGCACATTGACATGACTATTCCTTACAAAGCTTAACCCGG 660
DB 280 VALGINTYRGLYSPROGLINVAIHISILEGLINMETHTYRPROLEUNGINGLYLEUTHARG 299
QY 661 GAAGGGAGCCGCTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 300 GLUGLYASPRALPHESGLIUEUTHRCYSGIUALAILELYLSPROGLINPROVALMETVAL 319
QY 721 ACTTGGGTGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 320 THRTYRVALARGVALASPARGLUMETPROGLINHISALVALLEUSERTGLYPROASINLEU 339
QY 781 TTGATCATATACCTAAACAAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 340 PHEILEASNINLEUASNLYSTHNASPSNGLYTHRYARGCYSGIUALASERASNILE 359
QY 841 GTGGGGAAGCTCAGTGGATATATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 360 VALGILYVALHISASERASPTYRMELEUTYVALITYRSPROPTHTHTHLEPTIO 379
QY 901 CCTCCCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 960
DB 380 PROPTHT 399
QY 961 ACA-----GATTCGCCAGCAGGTGAAGAGGC 987
DB 400 THRASPTHT 1008
QY 988 TCGATCAGGCGCAGTGCATC 1008
DB 420 THRTILEGLYVALAVASPHIS 426

RESULT 5
Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DE 2900073606RIK protein.
GN IGSF4 OR 2900073606RIK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HIPOCAMPLUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,


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QY 388 GCTATGGCCAGCAAGCCAGCCAGCATATCAGTGTGTTCAAAGGAGCAACAGACCTAAA 447
    |||
Db 21 AlamelaserlyspProalThrThrIleGrpPheLysglYasnLysglLueLys 40
QY 448 GCGAAATCGGAGGTGGGAAGAGTGTGTGACATGTACACTGTGACCACTGACCTATGCTG 507
    |||
Db 41 GilysserGlualGluglUtrPserAspMetyrThrValThrSerGlnLeuMetLeu 60
QY 508 AAGGTGCACAGAGAGAGCATGGGGTCCAGTGTCTGCGAGTGGAGCAACCCCGCGGTC 567
    |||
Db 61 LysValHisLysglUaspAspGlyValProValIleCysGlnValGlnHisProAlaVal 80
QY 568 ACTGGAACCTGCAGACCCAGCGGTATCTAGAACTAGATATAAGCCTCAAGTGCACATT 627
    |||
Db 81 ThrGlysnLeuGlnThrGlnArgTyLeuGlnValGlnIlyrLysProGlnValHisIle 100
QY 628 CAGATGACTATTCCTCTACAAAGGCTTAACCCGGGAAGGGAGCGGCTTGAGTTAACTATG 687
    |||
Db 101 GlnMetThrTyrrProLeuGlnGlyLeuThrArgGlnGlyAspAlaPheGlnLeuThrCys 120
QY 688 GAAGCCATCGGGAAGCCCGCAGCTGTGATGTAACCTGGGAGAGTGCAGATGAGAATG 747
    |||
Db 121 GluAlaIleGlyLysProGlnProValMetValThrTriPalaArgValAspAspGlnMet 140
QY 748 CCTCAACAGCCGCTACTGTCTGGGCCCAACCTGTTCATCAATAACCTAAACAAACAGAT 807
    |||
Db 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnLeuAsnLysThrAsp 160
QY 808 AATGGTCAATACGCGCTGTGAAGCTCAACATAGTGGGAAAGCTGCATCGATATATG 867
    |||
Db 161 AsnGlyThrTyrrArgCysGlualAspAsnIleValGlyLysAlaHisSerAspTyrrMet 180
QY 868 CTGTATGTATACATCCCGCCACACACTATCCCTCCACCAACACACACACACACAC 927
    |||
Db 181 LeuTyrrValLysrProPrrProThrThrIlePrrProThrThrThrThrThrThrThr 200
QY 928 ACCACCAACCAACCAACCAATCTTACCATCATCAGATTCGCCAGAGAGGTGAAGAAGC 987
    |||
Db 201 ThrThrThrThrThrThrThrThrThrThrIleLeuThrIleIleThrAspSerArgAlaGlyGlnGly 220
QY 988 TCGATCGGCGCAGTGGATCAT 1008
    |||
Db 221 ThrIleGlyAlaValAspHis 227

RESULT 7
Q90YL4 PRELIMINARY: PRT: 306 AA.
AC O90YL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Adhesion protein RA175C.
GN IGSP4 OR RA175C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBITaxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouraku Y., Momoi M.,
RA Momoi T.;
RT "RA175, a novel neuron specific adhesion protein.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021966; BAA87916.1;
DR MGD: MGI:1889272; Igsf4.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_C2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00294; 4; 1m; 1.
DR SMART: SM00408; IgC2; 1.

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DR SMART; SM00410; Ig-like; 1.
KW Immunoglobulin domain.
SO SEQUENCE 306 AA; 33522 MW; A4CE37B0F2354D5 CRC64;

Alignment Scores:
Pred. No.: 1.55e-93 Length: 306
Score: 1157.50 Matches: 222
Percent Similarity: 94.12% Conservative: 2
Best Local Similarity: 93.28% Mismatches: 3
Query Match: 64.27% Indels: 11
DB: 11 Gaps: 1

US-09-778-187b-1_copy_130_1137 (1-1008) x Q90YL4 (1-306)
QY 328 ATGATCGATATCCGGAAGAAGACACTGCGGTGAAGTGAAGATTAAGTCAACTGCAT 387
    |||
Db 1 MetIleAspIleGlnLysAspThrAlaValGlnGlyLutGlnIleGlnValAsnGlyThr 20
QY 388 GCTATGGCCAGCAAGCCAGCCAGCATATCAGTGTGTTCAAAGGAGCAACAGACCTAAA 447
    |||
Db 21 AlamelaserlyspProalThrThrIleArgTrpPheLysglYasnLysglLueLys 40
QY 448 GCGAAATCGGAGGTGGGAAGAGTGTGTGACATGTACACTGTGACCACTGACCTATGCTG 507
    |||
Db 41 GilysserGlualGluglUtrPserAspMetyrThrValThrSerGlnLeuMetLeu 60
QY 508 AAGGTGCACAGAGAGAGCATGGGGTCCAGTGTCTGCGAGTGGAGCAACCCCGCGGTC 567
    |||
Db 61 LysValHisLysglUaspAspGlyValProValIleCysGlnValGlnHisProAlaVal 80
QY 568 ACTGGAACCTGCAGACCCAGCGGTATCTAGAACTAGATATAAGCCTCAAGTGCACATT 627
    |||
Db 81 ThrGlysnLeuGlnThrGlnArgTyLeuGlnValGlnIlyrLysProGlnValHisIle 100
QY 628 CAGATGACTATTCCTCTACAAAGGCTTAACCCGGGAAGGGAGCGGCTTGAGTTAACTATG 687
    |||
Db 101 GlnMetThrTyrrProLeuGlnGlyLeuThrArgGlnGlyAspAlaLeuGlnLeuThrCys 120
QY 688 GAAGCCATCGGGAAGCCCGCAGCTGTGATGTAACCTGGGAGAGTGCAGATGAGAATG 747
    |||
Db 121 GluAlaIleGlyLysProGlnProValMetValThrTriPalaArgValAspAspGlnMet 140
QY 748 CCTCAACAGCCGCTACTGTCTGGGCCCAACCTGTTCATCAATAACCTAAACAAACAGAT 807
    |||
Db 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnLeuAsnLysThrAsp 160
QY 808 AATGGTCAATACGCGCTGTGAAGCTCAACATAGTGGGAAAGCTGCATCGATATATG 867
    |||
Db 161 AsnGlyThrTyrrProCysGlualAspAsnIleValGlyLysAlaHisSerAspTyrrIle 180
QY 868 CTGTATGTATACATCCCGCCACACACTATCCCTCCACCAACACACACACACACAC 927
    |||
Db 181 LeuTyrrValLysrProPrrProThrThrIlePrrProThrThrThrThrThrThrThr 200
QY 928 ACCACCAACCAACCAACCAATCTTACCATCATCAGATTCGCCAGAGAGGTGAAGAAGC 983
    |||
Db 201 ThrThrThrThrThrThrThrThrThrThrIleIleThrAspThrThrAlaThrThrGluPro 220
QY 964 -----GATCCGAGCAGAGTGAAGAGTGCATATCGGCGACGATCAT 1008
    |||
Db 221 AlaValHisAspSerArgAlaGlyGlnGlyThrIleGlyAlaValAspHis 238

RESULT 8
Q90YL6 PRELIMINARY: PRT: 295 AA.
AC O90YL6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Adhesion protein RA175A.
GN IGSP4 OR RA175A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db 121 GlnAlaIleGlyLysProGlnProValMetValThrIrrValArgValAspSgluMet 140
QY 748 CCTCAACAGCCGCTACTGTCTGGGCCCAACCTGTTTCATCATTAACCTAAACAAAACAGAT 807
Db 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnAsnLeuAsnLysThrAsp 160
QY 808 AATGATCATATCCGCTGTGAAGCTTCAAACTAGTGGGGAAGAGCTCACTCGATTATATG 867
Db 161 AsnLysThrTyrrProGlyGlnAlaSerAsnIleValGlyLysAlaHisSerAspTyrIle 180
QY 868 CTGATGATATGATCCGCCCAACTATCCCTCTCCCAACAACACACACACACCC 927
Db 181 LeuTyrrValIrrAspThrThrThrIle-----LeuThrIleIle 194
QY 928 ACCACACACACACACACACATCTTACCATCATCATCAGATTCGCGAGAGTGAAGAGGC 987
Db 195 ThrAspThrThrIleThrThrGluProAlaValHisAspSerAlaGlyGluGluGly 214
QY 988 TCGATCAGGCGAGTGATCAT 1008
Db 215 ThrIleGlyAlaValAspHis 221

RESULT 10

O9QYL3 PRELIMINARY; PRT; 278 AA.
AC O9QYL3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RAI175N.
GN IGSF4 OR RAI175N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
RA Momoi T.;
RT "RAI175, a novel neuron specific adhesion protein.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021967; BAB87917.1; -.
DR MGD: MGI:1889272; IGSF4.
DR InterPro: IPR003598; Iq_C2.
DR InterPro: IPR003600; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003585; Neurexin-Like.
DR Pfam: PF00047; Iq_2.
DR SMART: SM00294; Iq_1m; 1.
DR SMART: SM00408; IqC2; 1.
DR SMART: SM00410; Iq_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;

Alignment Scores:

Pred. No.: 8.03e-82 Length: 278
Score: 1024.50 Matches: 198
Percent Similarity: 88.55% Conservative: 3
Best Local Similarity: 87.22% Mismatches: 9
Query Match: 56.89% Indels: 17
DB: 11 Gaps: 1

US-09-778-187b-1_copy_130_1137 (1-1008) x O9QYL3 (1-278)

QY 328 ATGATCATATTCAGAAAGACATCGCGGTGAGAGTGAGAGATTGAGTCACTGCATC 387
Db 1 MetIleAspIleGlnLysAspThrAlaValGluGlyGluIleGluValAsnCysThr 20
QY 388 GCTATGGCCGCAAGCCAGCAGCATATCAGGTGCTTCAAGGAACACAGAGCTTAA 447
Db 21 AlMetAlaSerLysProAlaThrThrIleArgTrrPheLysGlyAsnLysGluLeuLys 40

QY 448 GCGAATCGAGGTGGAAGAGTGTGACAGATGTACACTGTGACCACTGATGCTGTG 507
Db 41 GlyLysSerGluValGluGluThrIrrPserAspMetTyrThrValIrrSerGlnLeuMetLeu 60
QY 508 AAGGTGCACAAAGAGAGAGATGGGGTCCAGTGTATGTCAGAGTGGAGCAACCTCGCGTC 567
Db 61 LysValHisLysGlnAspAspGlyValProValIleCysGlnValGlnHisProAlaVal 80
QY 568 ACTGAAACCTGCAGACCCAGCCGCTATCTAGAACTAGATTAAGCTCAAGTGCACATT 627
Db 81 ThrLysAsnLeuGlnThrGlnArgTyrLeuGlnValGlnTrrLysProGlnValHisIle 100
QY 628 CAGATGACTTATCTCTTACAAAGGCTTAAACCCGGAGAGGAGCGGCTTGAGTTAACTATG 687
Db 101 GlnMetThrTyrrProLeuGlnGlyLeuThrArgGluGlnLysPalalaGluLeuThrCys 120
QY 688 GAACCCATCGGGAAGCCCAACCCCTGTATGTATGTTACCTGGGTGGAGAGTCGATGAGAAATG 747
Db 121 GlnAlaIleGlyLysProGlnProValMetValThrIrrValArgValAspSgluMet 140
QY 748 CCTCAACAGCCGCTACTGTCTGGGCCCAACCTGTTTCATCATTAACCTAAACAAAACAGAT 807
Db 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnAsnLeuAsnLysThrAsp 160
QY 808 AATGATCATATCCGCTGTGAAGCTTCAAACTAGTGGGGAAGAGCTCACTCGATTATATG 867
Db 161 AsnLysThrTyrrProGlyGlnAlaSerAsnIleValGlyLysAlaHisSerAspTyrIle 180
QY 868 CTGATGATATGATCCGCCCAACTATCCCTCTCCCAACAACACACACACACCC 927
Db 181 LeuTyrrValIrrAsp----- 185
QY 928 ACCACACACACACACACACATCTTACCATCATCATCAGATTCGCGAGAGTGAAGAGGC 987
Db 186 -----ThrThrAlaThrThrThrGluProAlaValHisAspSerAlaGlyGluGluGly 203
QY 988 TCGATCAGGCGAGTGATCAT 1008
Db 204 ThrIleGlyAlaValAspHis 210

RESULT 11

ID O8R464 PRELIMINARY; PRT; 388 AA.
AC O8R464;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Membrane glycoprotein.
GN TSL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SVJ;
RA Fukami T., Maryama T., Murakami Y.;
RT "Identification of a murine ortholog of the TSLC1-like gene 2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY059394; AAL29692.1; -.
SQ SEQUENCE 388 AA; 42723 MW; 8E3A9DF1C3B9D23E CRC64;

Alignment Scores:

Pred. No.: 2.58e-46 Length: 388
Score: 622.00 Matches: 123
Percent Similarity: 61.06% Conservative: 62
Best Local Similarity: 40.59% Mismatches: 112
Query Match: 34.54% Indels: 6
DB: 11 Gaps: 3

US-09-778-187b-1_copy_130_1137 (1-1008) x O8R464 (1-388)

QY 10 GGTGATGGCGCAAGATCTGTTTACGAAAGACGTGACAGTGATCGAGGAGAGCTTGCACCC 69


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Db 161 ThrValArgPheArgValAspArgLysAspArgLysIleIleIleCysGlnAlaGln 180
QY 556 CACCCGCGGCTCACTGGA-----AACCTGCAGACCCGCGGTATCTGAGATCACTGAT 609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AsnGlnAlaLeuProSerGlyHisSerLysGlnThrGlnValLeuAspValGlnIyr 200
QY 610 AAGCTCAAGTGCACATTACATGATGATCTTACAGAGCTTAAACCCGGGAAGGAGC 669
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 SerProThrAlaArgIleHisAlaSer-----GlnAlaValAlaArgGluGlyAsp 217
QY 670 GCGCTGATGATACATGATGAGGAGCCATGGGAGGCCCGCTGTGATGATGATGATGATG 729
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 ThrLeuValLeuThrCysAlaValThrGlyAsnProArgProAsnGlnIleArgITrpsn 237
QY 730 AGAGTCGATGATGAATATGCTCAACACGCCCTACTGTCTGGGCCCAACCTGTATCAAT 789
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 ArgGlyAsnGlnSerLeuProGluArgAlaGlnAlaValGlyGluThrLeuThrLeuPro 257
QY 790 AACCTAAACAACACGATATGATGATGATGATGATGATGATGATGATGATGATGATG 849
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 GlyLeuValSerAlaAspAsnGlyThrThrCysGlnAlaSerAsnLysHisGlyHis 277
QY 850 GCTACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 AlaArgAlaLeuThrValLeuValValThrGlyGlnSerArgLeuArgProThrGluGly 297
QY 895 -----ATCCCTCTCCCAACAACACACACACACACACACACACACACACACACAC 945
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 GlyGlyGlyAlaProAspProGlyAlaValValGlnAlaGlnThrSerValProThrAla 317
QY 946 ATCCTT 951
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 IleVal 319

RESULT 13
Q99N28 PRELIMINARY; PRT; 396 AA.
AC Q99N28;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein).
GN NECTN OR TSL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RT "Cloning and expression analysis of novel mouse cDNA encoding a
RL membrane protein."
RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SVJ;
RA Fukami T., Mauryama T., Murakami Y.;
RT "Identification of a murine ortholog of the TSL1-like gene 1."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF195662; AAG3584.1; -
DR EMBL: AY059393; AAL29691.1; -
DR MGD: MGI:2137858; Nect1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_3.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; IG_Like; 2.
KM Immunoglobulin domain.
SQ SEQUENCE 396 AA; 42964 MW; C1ADP8B57D141F3A CRC64;

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Alignment Scores:
Pred. No.: 5,12e-34 Length: 396
Score: 482.50 Matches: 110
Percent Similarity: 55.63% Conservative: 63
Best Local Similarity: 35.37% Mismatches: 119
Query Match: 26.79% Indels: 19
DB: 11 Gaps: 7

US-09-778-187b-1_copy_130_1137 (1-1008) x Q99N28 (1-396)
QY 13 GATGGGAGATCTGTTTACGAAGACGTGACATGATGCGAGGAGAGGTTGCGACATC 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 AspAspSerGlnProThrProThrSerAspGlnThrValAlaGlnGlyThrValLeu 46
QY 73 AGTGGCAAGTCAATTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 LysCysGlnValLysAspRnHisGlnAspSerSerLeuGlnTrpSerAsnProAlaGln 66
QY 133 ACCATTATTTTCAAGGACCTTCAGGCTTTTGAAGACAGACAGGTTTCAAGTTGTAATTT 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 ThrLeuThrPheGlyGlnLysArgAlaLeuArgAspAsnArgIleGlnLeuValSerSer 86
QY 193 TCTGACAGTGAACCTCAAGTATCATTTGACAAACCTTCATTTCTGATGAAGAAATAC 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 ThrProHisGlnLeuSerIleSerIleSerIleSerIleSerIleSerIleSerIleSer 106
QY 253 TTTTGCACAGTCTTATACCGATCCCGACAGGAAAGTTAACCACATCAGATCGTCTGTC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 107 ThrCysSerIlePheThrMetProValArgThrAlaLysSerLeuValThrValLeuGly 126
QY 313 CCACACGTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 IleProGlnLysProIleIleThrGlyThrLysSerSerLeuArgGlnLysGluThrAla 146
QY 373 GAATGCAACTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 ThrLeuAsnGlnSerGlnSerGlySerIleSerProAlaIleGlnLeuThrThrArgLysGly 166
QY 433 AACACAGAGCTAAAGAGC---AAATCGAGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGA 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 167 AspGlnGlnLeuHisGlnLysArgGlnThrArgIleGlnGlnLysProAsnGlnLysThrPhe 186
QY 484 ACTGTACACAGTCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 543
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 ThrValSerSerSerValSerPheGlnValThrArgGlnLysAspArgGlyAlaAsnIleVal 206
QY 544 TGCAGGATGAGAGCACCCTGGGCTGATGGA---AAGCTGACAGACCCAGCGGTATCTGA 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 CysSerValAsnHisGlnSerLeuLeuLysGlyAlaAspArgSerThrSerGlnArgIleGln 226
QY 601 GTACAGTATGAAGCTCAAGTGCACATTCAGATGACTTATCTGTACAAAGCTTAAACCCG 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 ValLeuThrThrProThrAlaMetIleArg-----ProGluProAlaHisProArg 243
QY 661 GAAGGAGACGGCTTGAAGTTAAATGTAAGCCATCGGGAAGCCCAACCTGTGATGTA 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 GluLysGlnLysLeuLeuLeuHisCysGlnGlyArgLysAsnProValProGlnGlnIyr 263
QY 721 ACTGGGATGAGAGTGCATGATGAATGAGCT-----CAACAGCGCGTATGCTGT 768
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 264 ValTrpValLysGlnLysSerGlnProProLeuLysMetThrGlnLysLeuAlaLeuIle 283
QY 769 GCGCCCAACCTGTTCATCAATTAACCTTAACAAACAGATGATGATGATGATGATGATG 828
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 PhePro-----PheLeuAsnLysSerSerPheGlyThrGlyCysThr 298
QY 829 GCTTCAAAACATAGTGGGAAAGCTCACTCGATTAATGCTGATGATGATGATGATGATG 888
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 AlaThrSerAsnMetGlySerGlyThrAlaLysThrPheThrLeuAsnValAspProSer 318
QY 889 ACAACATATCTCTCTCCCAACAACACACACAC 921
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 -----ProValProSerSerSerThr 326

```

RESULT 14					
ID	Q9UJPI	PRELIMINARY:	PRT:	432 AA.	
AC	Q9UJPI:				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	BK134P22.1 (Novel protein similar to mouse IMMUNOSUPERFAMILY protein BL2) (NECTIN-like protein 1).				
GN	BK134P22.1 OR NECL1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxId=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Baggaley C.;				
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	Zhou Y., Du G., Yuan J., Qiang B.;				
RA	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; AL035403; CAB56227.1; -				
DR	EMBL; AF062733; AAB1540.2; -				
DR	InterPro: IPR003598; IG_c2.				
DR	InterPro: IPR003600; IG_1ike.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003585; Neurexin-like.				
DR	pfam; PF00047; Ig_3.				
DR	SMART; SM00294; 4.Im; 1.				
DR	SMART; SM00408; IGC2; 1.				
DR	SMART; SM00410; IG_1like; 2.				
KW	Immunoglobulin domain.				
SO	SEQUENCE 432 AA; 47020 MW; AC474EFBC4C518C CRC64;				
Alignment Scores:					
Pred. NO.:	7,29e-33	Length:	432		
Score:	469.50	Matches:	105		
Percent Similarity:	55.96%	Conservative:	64		
Best Local Similarity:	34.77%	Mismatches:	122		
Query Match:	26.07%	Indels:	11		
DB:	4	Gaps:	6		
US-09-778-187B-1_COPY_130_1137 (1-1008) x Q9UJPI (1-432)					
OY	28 TTTTACGAAGACGTCGACGTATCGAGGGAGAGGTTGCCACCATCACTTGCCAAAGTAAT	87			
Dd	:::::	:::			
Dd	TTPThrSerAspGluThrIValAlaGlyIuThyValValLeuLysCysGlnValLys	87			
OY	88 AAGATGACGACTCGTGCATTCACTGACTGAATCCAAAGCGAGACCATTTATTTCAGG	147			
Dd	:::				
Dd	AspHisGluAspSerSerLeuGlnTrpSerAsnProAlaGlnGlnTrpLeuTyPhcGly	107			
OY	148 GACATTGACGCGCTTGAAGAGACAGAGGTTTCAGTGGTAATTTTTTAGACAGTAAC	207			
Dd	::: :::::	:::			
Dd	GluLysArgAlaLeuAlaArgAdaRsnAlaGlyIleGlnLeuValThrSerThrPrroHnIsGluLeu	127			
OY	208 AAGATGATATTGACAACAGCTGTCAATTTTGTGATAAGAGAGATCTTTGGCAAGCTAT	267			
Dd	:::				
Dd	SerIleSerIleSerAsnValAlaLeuValAspRinGluIuTyThrCysSerIlePhe	147			
OY	268 ACCGATGCCSCCAAGGAAGATTACACSSCATGCAAGTCGTCGGTCCGACACAGTAATCTG	327			
Dd	:::::				
Dd	ThrMetProValAlaGlyThrAlaLysSerLeuValItyValIleuGlyIleProGlnLysPro	167			
OY	328 ATGATGCAATTCACGAAGAAGACACTGCGGTGTGAAGSTGAGAGATTTGAATGCAACTGAC	387			
Dd	::: ::: :::::				
Dd	IleIleThrGlyTyuLysSerSerLeuAspGlyIuAspRinThrAlaThrIleAsnCyGln	187			
OY	388 CSTATGGCCACCAAGCCAGCCACACATATCAAGTGGTGTTCAAAGGAACACAGASTAAA	447			
Dd	:::				
Dd	SerSerGlySerLysVsrProAlaValAlaArgValuThrTrpArgLysGlnGlnLysHnIs	207			

QY	448	GGCAAA---TCGGAGGCGGAGGACGTGGTCAGAC-----ATGACATCTGGACACGACG	498
Db	208	GIUUPPProthirArq11EgInglAsProsm1yLysThrPhehrNalSerSer	227
QY	499	CTGATGCTGGAAGGCGCACAAAGAGACGATGGGGTCCAGTGAATTCGCCAGTGGAGAC	558
Db	228	ValThrPheInValThrArgGIuAsPaspRlyAlaSerIleValCysSerAlaNH1s	247
QY	559	CCTGGCGTCACTGGA---AACCTCAGACCCAGCGGATATTCAGAGTACAGTAAAGCT	615
Db	248	GIUSerIleuLysGIuAlaAsPArgSerThrSerIlnArq11EgInuValLeuYrThrPro	267
QY	616	CAAGGCGCATTCGAGATGACTTATGCTCTACAAAGCTTAAACCGGGAGGAGCGCGCTT	675
Db	268	ThrAlaMetIleArgProAsProPro-----HisProArgGIuGIuInLysLeu	284
QY	676	GAGTTAACATGTGAAGCCATCGGAGAGCCGCCACCGCTGTGATGGTAACTTGGTGAGATC	735
Db	285	LeuIleuHisCysGIuGIuArgGIuAsnProValProInGIuInYrLeuTrpGIuLys---	303
QY	736	GATGATGAAATGCGCTCAACACGCCGCTACTGCTGGGCCCAACCTGTTCATCAATCACTA	795
Db	304	GIuGIuSerValProProLeuLysMetThrCInGIuSerAlaLeuIlePheProPheLeu	323
QY	796	AACAAACAGATTAATGGTACATACCGCGTCAGACCTTCAAAACATAGCGGGAAGCTCAC	855
Db	324	AsnLysSerAspSerGlyThrTyGIuCysThrAlaThrSerAsnGlySerTyLys	343
QY	856	TGCGATTATATGCTGTATGTATGATACGATCCGCCCAACATATCCCTCCCTCCACACACAC	915
Db	344	AlaTyTyTyThrLeuAsnValAlaAsnAspSer-----ProValProSerSerSer	360
QY	916	ACCACC 921	
Db	361	SerThr 362	
RESULT 15			
QY	99D006	PRELIMINARY;	PRT: 549 AA.
AC	Q9D006;		
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;		
RC	MEDLINE=21085660; PubMed=11217851;		
DT	01-JUN-2001 (TREMBLrel, 17, Created)		
DT	01-JUN-2001 (TREMBLrel, 17, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)		
DE	2610301B19Rik protein.		
GN	2610301B19Rik.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Eutelestomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;		
RC	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinaawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adechi J., Fukuda S.,		
RA	Alawa K., Iwase H., Nishi K., Kiyosawa H., Kondo S., Yamana I.,		
RA	Saito T., Okazaki Y., Gobjori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Glasl C., King B., Kochia H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		

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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:39:05 : Search time 48.25 seconds
(without alignments)
5567.528 Million cell updates/sec

Title: US-09-778-187b-1_COPY_130_1137

Perfect score: 1801

Sequence: 1 atccccacagtgatcgggca.....cgatcagggcagcgatcatc 1008

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=framer_n2p_model -DEV=xlp
-O/csgn2.1/USPRO.spool/US09778187/runat.20112002_073629_26303/app_query.fasta_1.2318
-DB=A.Geneseq.101002 -OPMT=fastan -SUFFIX=tag -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09778187.ecgn1.1.71.runat.20112002_073629_26303 -NCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NBG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEDOUT=120
-NARN_TIMEDOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A.Geneseq.101002.*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1761	97.8	402	22	AAM23691	Human EST encoded
2	1761	97.8	440	20	AAV17830	Human PRO355 prote
3	1761	97.8	440	21	AAAB01321	Human PRO355 polyp
4	1761	97.8	440	22	AAU29040	Human PRO polypept
5	1761	97.8	442	21	AAAB25619	Protein encoded by
6	1761	97.8	442	21	AAV94341	Human cell surface
7	1761	97.8	442	21	AAV45092	Human lymphoid der
8	1761	97.8	442	23	AAE19887	Human tumour suppr
9	1741	96.7	423	21	AAV45093	Beta-lymphoid der
10	1704	94.6	364	21	AAAB25866	Protein encoded by
11	1612.5	89.5	443	22	AAAB8427	Human membrane or
12	1591	88.3	414	21	AAV53028	Human secreted pro
13	1167.5	64.8	229	21	AAAB25593	Protein encoded by
14	629	34.9	387	22	AAV78418	Human protein SEQ
15	623.5	34.6	444	20	AAV33741	Beta-secretase. H
16	623.5	34.6	444	22	AAV47251	Beta-secretase. H
17	604	33.5	388	22	AAAB1897	Human P22162.1 hom
18	597	33.1	388	22	AAV79402	Human protein SEQ
19	578.5	32.1	404	23	AAAB6677	Human novel polype
20	576.5	32.0	404	22	AAAB61142	Human NOV12 protei
21	482.5	26.8	398	21	AAV69287	Mouse brain immun
22	482.5	26.8	404	22	AAE00868	Mouse acid sequenc
23	475.5	26.4	564	21	AAV94405	Human ACAM4/19G4-F
24	473.5	26.3	598	21	AAV94404	Human ACAM6/19G4-F
25	471.5	26.2	368	21	AAV94405	Human ACAM4/19G1-F
26	471.5	26.2	398	19	AAAB80405	A secreted protein
27	471.5	26.2	398	20	AAV29592	Human MBGP1 protei
28	471.5	26.2	398	20	AAV13358	Amino acid sequenc
29	471.5	26.2	398	21	AAV94403	Human ACAM cellula
30	471.5	26.2	398	21	AAV69288	Amino acid sequenc
31	471.5	26.2	398	21	AAV45095	Human LDCA2 bindin
32	471.5	26.2	398	22	AAV12345	Human PRO258 polyp
33	471.5	26.2	398	22	AAAB80226	Human PRO358 prote
34	471.5	26.2	398	22	AAAB53083	Human angiolegensis
35	471.5	26.2	398	23	AAAB91823	Human polypeptide
36	471.5	26.2	398	23	AAAB95444	Human angiolegensis
37	471.5	26.2	398	23	AAAB84838	Human PRO258 prote
38	471.5	26.2	413	22	AAE00867	Human brain immuno
39	469.5	26.1	367	22	AAAB51281	Human secreted pro
40	469.5	26.1	367	22	AAAB51280	Human secreted pro
41	469.5	26.1	432	21	AAV94402	Human ACAM cellula
42	469.5	26.1	432	21	AAV69286	Amino acid sequenc
43	469.5	26.1	432	21	AAV45094	Human LDCA2 bindin
44	469.5	26.1	432	22	AAAB50413	Human secreted pro
45	459	25.5	433	21	AAV53272	Human Beat-1-like 1

ALIGNMENTS

RESULT 1
ID AAM23691 standard; Protein; 402 AA.
AC AAM23691:

DE Human EST encoded protein SEQ ID NO: 1216.
DT 12-OCT-2001 (first entry)

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.

OS Homo sapiens.
XX WO200154477-A2.
XX

PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001MO-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98350.
XX
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX
PS Claim 20; Page 877-878; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
XX Sequence 402 AA;
SQ

Alignment Scores:
Pred. No.: 7.61e-151 Length: 402
Score: 1761.00 Matches: 336
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 22 Gaps: 0

US-09-778-187b-1_COPY_130_1137 (1-1008) x AAM23691 (1-402)
QY 1 ATCCCCACAGGTGATGGGACAGATCTGTTTACGAAGAAGCTGACAGTGCAGGAGAG 60
DB 39 11leerthrghlyspgylglnasnleuphetrlyspalrthrvalilegluglu 58
QY 61 GTTGGCCATCATGTTGCCAAGTCATTAAGAGTACACACTCTGTGATTCTACTGAAT 120
DB 59 ValAlaThrIleSerCysGlnValAsnLysSerAspSerValIleGlnLeuAsn 78
QY 121 CCCAAGCAGCAGACCATTTATTTTCAGGACTTCAGCCCTTGAAGGACAGAGTTTCAG 180
DB 79 ProAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 98
QY 181 TTGCTGAATTTTCTACAGTGAATCAAGTATCATTTGACAAAGCTCTCAATTTCTGAT 240
DB 99 LeuLeuAsnPheserSerSerGlnLeuLysValSerLeuThrAsnValSerIleSerAsp 118
QY 241 GAAGGAAGATACTTTTGGCAGCTCTATACGATCCCCACAGGAAGTTACCCACCATC 300
DB 119 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 138
QY 301 ACAGTCTGTGGTCCACACAGTAAATCTGATGATTCACGAAGAAGCAGCTGGGTGAA 360
DB 139 ThrValLeuValProProAlaGlnLeuMetIleAspIleGlnLysAspThrAlaValGlu 158
QY 361 GGTGAGAGATTGAGTCAACTGCATCTATGAGCCAGCAAGCCAGCCAGTATCAGG 420
DB 159 GlyGluGlnIleGluValAsnGlyThrAlaMetAlaSerLysProAlaThrThrIleArg 178
QY 421 TGGTTCAAAGGGAACACAGAGCTAAAGGCAATCGAGGTGGAAGTGTGTACAGATG 480
DB 421 TGGTTCAAAGGGAACACAGAGCTAAAGGCAATCGAGGTGGAAGTGTGTACAGATG 480

DB 179 TrpPheLysGlyAsnThrGluLeuLysGlyLysSerGluValGluGluTyrSerAspMet 198
QY 481 TACACTGTGACACAGTCAAGCTGATGCTGAAGTGCACAAAGAGAGAGATGGGTCACAGT 540
DB 199 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGluAspArgValProVal 218
QY 541 ATCTGCCAGGTGAGACACCTCGGTCACAGTGAACCTGCAGACCCAGCCGATCTGA 600
DB 219 IleCysGlnValGlnHisProAlaValThrGlyAsnLeuGlnThrGlnArgTyrLeuGlu 238
QY 601 GTACAGTATAGCCTCAAGTCCACATCAAGTACTATCCCTACAAAGCTTACCCGG 660
DB 239 ValGlnTyrLysProGlnValHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 258
QY 661 GAAGGGAGCGGCTTGAGTTAATCATGTGAAGCCATCGGGAAGCCCAAGCCCTGATGCTA 720
DB 259 GluGlyAspAlaLeuGluLeuThrCysGluAlaIleGlyLysProGlnProValMetVal 278
QY 721 ACTTGGGTGAGAGTGCATGATGAATGCCTGCACAGCGCCGTACTGTCTGGGCCACCTG 780
DB 279 ThrTrpValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu 298
QY 781 TTCTCATATACCTTAACCAAAACAGATTAATGTCATACCGCTGTGAAGCTTCAACATA 840
DB 299 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGluAlaSerAsnIle 318
QY 841 GTGGGAAAGCTCACTCGGATTAATGCTGATATACGATCCGCCACAACTATCCCT 900
DB 319 ValGlyLysAlaHisSerAspTyrMetLeuTyrValIlyrasProProThrThrIlePro 338
QY 901 CTTCCCAACAAACATC 960
DB 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIle 358
QY 961 ACAGATTCGCGAGAGGTGAAGAGGCTCGATCGAGGACAGTTCAT 1008
DB 359 ThrAspSerArgAlaGlyGluGlySerIleArgAlaValAspHis 374

RESULT 2
AA17830
ID AAV17830 standard; Protein; 440 AA.
XX
XX AAV17830;
XX
XX 12-AUG-1999 (first entry)
XX
XX Human PRO355 protein sequence.
XX
XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder.
XX
XX Homo sapiens.
XX
XX WO9928462-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25108.
XX
XX
XX 25-FEB-1998; 98US-0075945.
XX 03-DEC-1997; 97US-0067411.
XX 11-DEC-1997; 97US-0069278.
XX 11-DEC-1997; 97US-0069334.
XX 11-DEC-1997; 97US-0069335.
XX 12-DEC-1997; 97US-0069425.
XX 16-DEC-1997; 97US-0069694.
XX 16-DEC-1997; 97US-0069696.
XX 16-DEC-1997; 97US-0069702.
XX 17-DEC-1997; 97US-0069870.
XX 17-DEC-1997; 97US-0069873.
XX 18-DEC-1997; 97US-0068017.
XX 05-JAN-1998; 98US-0070440.
XX 09-FEB-1998; 98US-0074086.

PR 09-FEB-1998: 98US-0074092.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WT:
 PI Yuan J;
 XX MPI: 1999-371118/31.
 XX N-PSDB: AAX80055.
 XX
 PT Nucleic acids encoding PRO secreted and transmembrane proteins
 XX
 XX Claim 12: Fig 27: 123pp: English.
 XX
 CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytoskeletal, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.

SO Sequence 440 AA:

Alignment Scores:

Pred. No.: 7,81e-151 Length: 440
 Score: 1761.00 Matches: 336
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.78% Indels: 0
 DB: 20 Gaps: 0

US-09-778-187b-1_COPY_130_1137 (1-1008) x AAY17830 (1-440)

QY 1 ATCCCAAGGATGAGGAGCAATCTGTTTACGAAAGACGTGACATGATCGAGGAGAG 60
 DB 37 IIEPOTHTGIIYASPEIYGLINASLEUPHERNLYASPAVALTHRVALLIEGLUGIYGLI 56
 QY 61 GTTGGACACATGATGTCGCAAGTCATTAAGAGTCCTGTGATTCAGCTACATGAAT 120
 DB 57 VALAATHRIISERCYSGLINVALSNLYSSEASPASERVALIIEGLINLEUASN 76
 QY 121 CCCAACAGCAGACACATTAATTATTCAGAGGACTTCAGSCCTTGTGAAGACAGAGTTTCAG 180
 DB 77 PROASNARGGLNTHRIETRYRHEARGASPRHEARGPROLEULYSASPERARGPHEGLN 96
 QY 181 TTGCTGAATTTTCTTAGCAGTGAAGTCAAGTAATTCATTCATTCATTCATTCATTCAT 240
 DB 97 LEULEUASNPHSE 116
 QY 241 GAAGGAAGTACTTTTGGCAGCTCTTACCGATCCCGCCAGAGAAAGTAAACCCACATC 300
 DB 117 GUGUGYARTRYRHECYSGLINLEUTYRTHASPRPROGLNGLNLSERYRTHRIITILE 136
 QY 301 ACAGTCTGCTGCCACACAGTATCTGATGATGATATTCAGAAAGACATCGCGGTGAA 360
 DB 137 THRVALLLEUVALPROFORARGASNLEUMETILEASPIIEGLINLYSPHRIALAVAILGI 156
 QY 361 GGTGACGACATTTGAAGTCACTGCTATGCGCAGAGAACGCCACACGACTATCAGG 420
 DB 157 GLYGLUGIUIIEGLIVALSNLYSTRALAMEVALSERLYSPROALATHRIITILEARG 176
 QY 421 TGGTTCAAGGGAACACACAGCTAAAGGCAATCGAGAGTGAAGAGTGCATGACATG 480
 DB 177 TTPRPELYSGIYASNTHRIULEULYSGLIYSESGIYVALGIUNLUTRPSERASPMET 196
 QY 481 TACACTGTACACAGTACGTGATGCTGAAGGTGCACACAGAGACGATGGGTCCAGTG 540
 DB 197 TYRTHTVALTHSERGLNLEUMETLEULYSVALHISLYSGLIUNASPRGLYVALIPROVAL 216
 QY 541 ATCTGCCAGGTGACAGACCCCTGGGCTCACTGGAAACCTGCACAGCCACGGGATTCAGAA 600

DB 217 IIECYSGLINVALGIUNHISPROALAVALTHRIYASNLEUGLINTHRGLNARGTRYLEUGLI 236
 QY 601 GFACATATTAAGCCTCAAGTGCACATTCAGATGATTCATTCCTTACAAAGCCTTAACCCGG 660
 DB 237 VALGINTYRLYSPROGLNVALHISIEGLINMETCTTRYRPROLEUGLNGIYLEUTHRIARG 236
 QY 661 GAAGGGAGCCGCTTGATGATTAACATGTGAAGCCATCGGGAAGCCCGACGCTGTGATGTA 720
 DB 257 GLUGIYASPRALALEUGLNULEUTHRICYSGLUALALIEGLIYASPRGGLNPROVALMETVAL 276
 QY 721 ACTTGGGTGAGAGTGCATGATGAATGCCCTCAACACGCCGCTACTGCTGTGGCCCAACTG 780
 DB 277 THTRPVVALARGVALASPRGLIMETPROGLNHISALAVALLEUSERGLYPROASNLEU 296
 QY 781 TTCATCATTAACCTTAACAAACAGATTAATGTGATACCGCTGTGAGCTTCAACATTA 840
 DB 297 PHEIIASNNSLEUASNLYSTRHASPASNGIYTHTRYARGYSGIUNLASERANILE 316
 QY 841 GTGGGAAAGCTCACTCGGATTAATGCTGTATGATAGCATCCGCCACACATATCCCT 900
 DB 317 VALGIYALAHISSEASPRTRYMETLEUTRYVALITYASPRPROPTHRIILEPRO 336
 QY 901 CCTCCCAACACACACACACACACACACACACACACACACACACATCTTACCATCATC 960
 DB 337 PROPTHRIETHRIETHRIETHRIETHRIETHRIETHRIETHRIETHRIETHRIETHRI 356
 QY 961 ACAGATTTCCGACAGGTGAAGAGGCTGCATCAGGCGACGTGATCAT 1008
 DB 357 THRASPERARGVALIEGLIUGIUGIYSERIIEARGALVALASPHIS 372

RESULT 3
 AAB01321
 ID AAB01321 standard: Protein; 440 AA.
 XX
 AC AAB01321:
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Human PRO355 polypeptide.
 XX
 KW PRO: membrane bound protein; secreted protein; PRO357; PRO327;
 KW PRO243; PRO715; PRO241; PRO23; PRO299; PRO233; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT
 FT Modified-site
 FT /note= "N-myristoylation site"
 FT 9..15
 FT Modified-site
 FT /note= "N-glycosylation site"
 FT 65..69
 FT Modified-site
 FT /note= "N-glycosylation site"
 FT 99..103
 FT Modified-site
 FT /note= "N-glycosylation site"
 FT 111..115
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 FT /note= "N-glycosylation site"
 FT 163..167
 FT Modified-site
 FT /note= "N-glycosylation site"
 FT 227..233
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 FT 233..240
 FT Modified-site
 FT /note= "tyrosine kinase phosphorylation site"
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 FT /note= "N-glycosylation site"
 FT 306..310
 FT Modified-site
 FT /note= "N-glycosylation site"
 FT 307..313
 FT Modified-site
 FT /note= "N-myristoylation site"
 FT 319..328
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 FT /note= "tyrosine kinase phosphorylation site"
 FT 365..371

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FT      411..417
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FT      427..433
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FT      428..432
FT      /note="N-myristoylation site"
FT      430..434
FT      /note="N-glycosylation site"
FT      WO200032776-A2.
XX
XX      08-JUN-2000.
XX
XX      01-DEC-1999; 99WO-US28301.
XX
XX      01-DEC-1998; 98WO-US25108.
XX      16-DEC-1998; 98US-0112850.
XX      22-DEC-1998; 98US-0113296.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
XX      Gerlitsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
XX      Hillan KJ, Kijavlin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX      MPI; 2000-412324/35.
XX      N-PSDB; AAA49563.
XX
XX      New human nucleic acids encoding secreted and transmembrane
XX      polypeptides, designated as PRO polypeptides, useful as pharmaceutical
XX      and diagnostic agents
XX
XX      Claim 12; Fig 24; 187pp; English.
XX
XX      New human nucleic acids encoding secreted and transmembrane
XX      polypeptides which are designated as PRO polypeptides are described
XX      The membrane-bound proteins have various industrial applications,
XX      including as pharmaceutical and diagnostic agents. The membrane-bound
XX      proteins can also be employed for screening of potential peptide or
XX      small molecule inhibitors of the relevant receptor/ligand interaction.
XX      Anti-PRO antibodies are useful for the affinity purification of PRO
XX      from recombinant cell culture or natural sources.
XX
XX      Sequence 440 AA:
XX
XX      Alignment Scores:
XX      Pred. No.: 7 81e-151 Length: 440
XX      Score: 1761.00 Matches: 336
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 97.78% Indels: 0
XX      DB: 21 Gaps: 0
XX
XX      US-09-778-187B-1_COPY_130_1137 (1-1008) x AAB01321 (1-440)
```

```
QY      181 TTGCTGAATTTTCTACAGTGAAGTCAAGTATCATTTGACAAACGTCATTTCTGAT 240
DB      |||
DB      97 LeuLeuAsnPhSerSerSerSerGluLeuLysValSerLeuThrAsnValSerIleSerAsp 116
QY      241 GAAGGAAGATATCTTTGGCAGCTCTATACCGATCCCGCAGGAAGTTACACGACATC 300
DB      |||
DB      117 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 136
QY      301 ACAGTCCGTCGCCACACCGTAATCTGATGTCATATCCGAAGAAGACATCGCGTGGAA 360
DB      |||
DB      137 ThrValLeuValProProAlaGlnLeuMetIleAspIleGlnLysAspThrAlaValGlu 156
QY      361 GGTGAGGAGATTGAAGTCAACCTGCATGCTATGGCCAGCAGCAGCCAGCAGCTATCAGG 420
DB      |||
DB      157 GlyGluGluIleGluValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg 176
QY      421 TGGTTCAAAGGGAACACAGACCTAAAGCAAAATCGAGGTGGAAGAGTGTGACAGATG 480
DB      |||
DB      177 TrpPheLysGlyAsnThrGlnLeuLysGlyLysSerGluValGlnGluTrpSerAspMet 196
QY      481 TACACTGTGACCACTGACCTGATGCTGATGAGGTGCACAAAGAGAGCATGGGCTCCACTG 540
DB      |||
DB      197 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspAspGlyValProVal 216
QY      541 ATCTGCAGGTGGAGACACCCCTGCGTCACTGGAACCTGCAGACCCAGCGGTATCTAGAA 600
DB      |||
DB      217 IleCysGlnValGlnHisProAlaValAlaThrGlnLysLeuGlnThrGlnAlaArgTyrLeuGlu 236
QY      601 GTACAGTATAGCCCTCAAGTGCACATTCAGATGACTTATCCTCTPACAGGCTTAACCCG 660
DB      |||
DB      237 ValGlnTyrLysProGlnValHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 256
QY      661 GAAGGGAGCGCGCTTGAAGTATACATGTGAGGCCATCGGGGAAGCCCGCTGTATGTA 720
DB      |||
DB      257 GluGlyAspAlaLeuGluLeuThrCysGluAlaIleGlyLysProGlnProValMetVal 276
QY      721 ACTTGGGTGAGAGTCGATGATGAATGCCCTCAACACCCCGTATGTCGGGCCAACCTG 780
DB      |||
DB      277 ThrTrpValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
QY      781 TTCATCAATTAACCTTAACAAACAGATATGTCATACCGCTGTGAACTTCAACATA 840
DB      |||
DB      297 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGluAlaSerAsnIle 316
QY      841 GTGGGGAAGCGTCCTCGGATTATATGCTGATGTCATACCATCCCGCACAACATACCT 900
DB      |||
DB      317 ValGlyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProThrThrIlePro 336
QY      901 CCTCCACAAACACACACACACACACACACACACACACACACACATCTTACCATCATC 960
DB      |||
DB      337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 356
QY      961 ACAGATTCGCCAGAGCTGAAGAAGGCTCGATCAGGCGACGTGATCAT 1008
DB      |||
DB      357 ThrAspSerArgAlaGlyGluGlySerIleArgAlaValAspHis 372
XX
XX      RESULT 4
XX      ID AAU29040 standard; Protein: 440 AA.
XX      AC AAU29040;
XX      DT 18-DEC-2001 (first entry)
XX      DE Human PRO polypeptide sequence #17.
XX      KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX      dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX      blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX      adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX      OS Homo sapiens.
```

XX WO200168848-A2.
XX
XX 20-SEP-2001.
XX
PF 28-FEB-2001: 2001WO-US06520.
XX
XX 01-MAR-2000: 2000WO-US05601.
PR 02-MAR-2000: 2000WO-US05841.
PR 03-MAR-2000: 2000US-187202P.
PR 06-MAR-2000: 2000US-186968P.
PR 14-MAR-2000: 2000US-189320P.
PR 14-MAR-2000: 2000US-189328P.
PR 15-MAR-2000: 2000WO-US06884.
PR 21-MAR-2000: 2000US-190828P.
PR 21-MAR-2000: 2000US-191007P.
PR 21-MAR-2000: 2000US-191048P.
PR 21-MAR-2000: 2000US-191314P.
PR 28-MAR-2000: 2000US-192655P.
PR 29-MAR-2000: 2000US-193032P.
PR 29-MAR-2000: 2000US-193053P.
PR 30-MAR-2000: 2000WO-US08439.
PR 04-APR-2000: 2000US-194449P.
PR 04-APR-2000: 2000US-194647P.
PR 11-APR-2000: 2000US-195975P.
PR 11-APR-2000: 2000US-196000P.
PR 11-APR-2000: 2000US-196187P.
PR 11-APR-2000: 2000US-196690P.
PR 11-APR-2000: 2000US-196820P.
PR 18-APR-2000: 2000US-198121P.
PR 18-APR-2000: 2000US-198585P.
PR 25-APR-2000: 2000US-199397P.
PR 25-APR-2000: 2000US-199550P.
PR 25-APR-2000: 2000US-199654P.
PR 03-MAY-2000: 2000US-201516P.
PR 17-MAY-2000: 2000WO-US13705.
PR 22-MAY-2000: 2000WO-US14042.
PR 30-MAY-2000: 2000WO-US14941.
PR 02-JUN-2000: 2000WO-US15264.
PR 05-JUN-2000: 2000US-209832P.
PR 28-JUL-2000: 2000WO-US20710.
PR 22-AUG-2000: 2000US-0644848.
PR 24-AUG-2000: 2000WO-US23328.
PR 08-NOV-2000: 2000WO-US30952.
PR 01-DEC-2000: 2000WO-US32678.
PR 20-DEC-2000: 2000WO-US34956.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX MPI: 2001-602746/68.
DR N-PSDB: AAS45941.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
XX Claim 11: Fig 34; 774pp; English.
XX
XX Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also

CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 440 AA:
Alignment Scores:
Pred. No.: 7, 81e-151 Length: 440
Score: 1761.00 Matches: 336
Best Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 22 Gaps: 0
US-09-778-187B-1_COPY_130_1137 (1-1008) x AAU29040 (1-440)
QY 1 ATCCCCACAGCTGATGGCGAATCTGTTACGAAGAGCTGACAGTGCAGGAGAG 60
DB |||
QY 37 ILePThrGlyAspGlyInAsnLeuPheThrLysAspValIleGluGlyGlu 56
DB |||
QY 61 GTTGGCAGCATCGTTGCCAAGTCAATAGAGTGAGCAGCTGTGATTCAGTCAAT 120
DB |||
QY 57 ValAlaThrIleSerCysGlnValAsnLysSerAspAspSerValIleGlnLeuAsn 76
DB |||
QY 121 CCCACAGCGACACATTTATTTTCAGGAGCTCAGCCCTTGAAGACAGCAGGTTTCAG 180
DB |||
QY 77 ProAsnArgGlnThrIleTyrrPheArgAspPheArgProLeuLysAspSerArgPheGln 96
DB |||
QY 181 TTGCTGAATTTTCTACAGCTGAAGTCAAGTATCATTCGAACAGTCTCATTTCTGAT 240
DB |||
QY 97 LeuLeuAsnPheSerSerSerSerGluLeuLysValSerLeuThrAsnValSerIleSerAsp 116
DB |||
QY 241 GAAGGAAGATACATTTTGGCCAGCTATACCGATACCCACAGGAAGTTCACCAACATC 300
DB |||
QY 117 GluGlyArgGlyrPheCysGlnLeuTyrrThraSPProGlnGlnSerTyrrThrIle 136
DB |||
QY 301 ACAGTCTGCTCCACACACACCTAATCTGATGATGATATCCAGAAGACACTGGCGTGA 360
DB |||
QY 137 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 156
DB |||
QY 361 GGTGAGAGAGATTGAAGTCAACTGACACTGCTATGAGCCAGCAAGCAGCAGCATATCAG 420
DB |||
QY 157 GlyGlnGluIleGluValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg 176
DB |||
QY 421 TGGTCAAGGAGAACACAGAGCTAAAGCAAAATCGAGGAGGAGAGAGTGTGCAGATG 480
DB |||
QY 177 TrpPheLysGlnAsnThrGluLeuLysGlyLysSerGluValGluGluTrpSerAspMet 196
DB |||
QY 481 TACACTGTGACACAGTCAAGTCAATGCTGAAGTGCACAAAGAGAGCAGTGGTCCAGTG 540
DB |||
QY 197 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspArgLysProVal 216
DB |||
QY 541 ATCTGCCAGGTGAGAGACACCTGGCGGTCTACTGGAACCTGCAGACCCAGCGTATCTGA 600
DB |||
QY 217 IleCysGlnValIleGluHisProAlaValThrGlyAsnLeuGlnThrGlnAlaGlyrLeuGlu 236
DB |||
QY 601 GTACAGTATTAAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 660
DB |||
QY 237 ValGlnTyrrLysProGlnValHisIleGlnMetThrTyrrProLeuGlnGlnLysLeuThrArg 256
DB |||
QY 661 GAAGGGAGCCGCTTGATTAACATGTAAGCCATCCGGAAGCCCAAGCCTGTGATGTGA 720
DB |||
QY 257 GluGlyAspAlaLeuGluLeuThrCysGluAlaIleGlyLysProGlnProValMetVal 276
DB |||
QY 721 ACTTGGGTGAGAGTCAATGTAATGTAATGCCCTCAACAGCCGCTACTGTGTGGCCCAACTG 780
DB |||
QY 277 ThrTrpValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
DB |||
QY 781 TTTCATCATTAACCTAAACCAACAGATATGTATACATACCGCTGTGAAGCTTCAACATA 840
DB |||
QY 297 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrrArgCysGlnAlaSerAsnIle 316
DB |||

QY	841	GGGGGAAAGCGCATCGGATATATAGCTGATATGATACGATCCCGACACATATCGCT	900
Db	317	VALGlyLysSAlAlAlHisSerAspTyrMetLeuLysValTyrAspProProlThrThrIlePro	336
QY	901	CTCCATCCATCATC	960
Db	337	ProProlThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle	356
QY	961	ACAGATTCGCCGAGCAGGTGAGAAAGGCTCGATCAGCGGACGATGATCAT	1008
Db	357	ThrAspSerArgAlaGlyGluGluGlySerIleArgAlaValAspHis	372
RESULT 5			
ID	AAB25619	standard; Protein: 442 AA.	
XX			
AC	AAB25619;		
XX			
DT	21-NOV-2000	(first entry)	
XX			
DE	Protein encoded by human secreted protein gene #11.		
XX			
KW	Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;		
KW	antihematic; dermatological; antiproliferative; antiarteriosclerotic;		
KW	anticancer; vulnerary; antiviral; antibacterial; antifungal;		
KW	immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;		
KW	multiple sclerosis; inflammatory disorder; inflammatory bowel disease;		
KW	Crohn's disease; nephritis; hyperproliferative disorder;		
KW	cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer		
KW	melanoma; lymphoma; wound healing; human.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200029435-A1.		
XX			
PD	25-MAY-2000.		
XX			
PE	27-OCT-1999; 99WO-US25031.		
XX			
PR	28-OCT-1998; 98US-0105971.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Ni J, Ruben SM, Olsen HS, Young PE, Kenny JT, Moore PA, Wei Y;		
PI	Greene JM;		
DR	WPI: 2000-387742/33.		
XX			
PT	Isolated nucleic acid molecules encoding human secreted proteins are		
PT	used for the prevention, amelioration and treatment of autoimmune,		
PT	inflammatory, hyperproliferative and cardiovascular disorders, cancer,		
PT	wounds, and infectious diseases.		
XX			
PS	Disclosure: Page 182-183; 803pp; English.		
XX			
CC	The present invention relates to 12 secreted human proteins and the		
CC	nucleotide sequences encoding them. The polynucleotide sequences given		
CC	in AA80606-480623 encode the 12 secreted protein sequences given in		
CC	AA825756-825593. The human secreted proteins have various activities		
CC	dependent on the tissues in which they are expressed. Examples of the		
CC	activities of the proteins include: Immunosuppressant;		
CC	anti-inflammatory; antiarthritic; antirheumatic; dermatological;		
CC	antiproliferative; antiarteriosclerotic; anticancer; vulnerary;		
CC	antiviral; antibacterial; and antifungal activity. The proteins,		
CC	polypeptides, agonists and antagonists may be used to treat prevent		
CC	and/or diagnose various disease, disorders and conditions examples of		
CC	which include: immune disorders e.g. Addison's disease, rheumatoid		
CC	arthritis, dermatitis, and multiple sclerosis; inflammatory disorders		
CC	e.g. inflammatory bowel disease, Crohn's disease and nephritis;		
CC	hyperproliferative disorders such as paraproteinaemias and purpura;		
CC	cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;		
CC	cancer e.g. melanoma and lymphoma. The proteins and polynucleotide		
CC	sequences may also be used in wound healing and the treatment of		

CC	infectious diseases. The human secreted protein gene #11 and protein		
CC	sequences are represented in sequences AAA0616 and AAB25586. Sequences		
CC	AAA06177-A80882 represent genes related to the secreted protein gene#11		
XX			
Sequence	442 AA;		
Alignment Scores:			
Pred. No.:	7.82e-151	Length:	442
Score:	1761.00	Matches:	336
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.78%	Indels:	0
Db:	21	Gaps:	0
US-09-778-187B-1_COPY_130_1137 (1-1008) x AAB25619 (1-442)			
QY	1 ATCCCCACAGGATGGGCGACAAATCTGTTACGAAAGACGTGACAGTGTGAGGAGAG	60	
Db	39 ILEPOTHTGILYASPGILGLASNEUHEPHERILYASPAVILTHRAVILLEGILGLY	58	
QY	61 GTTGGACATCAGTGGCCAGTCAATTAAGATGACGACTGTGATTCAGCTCAAT	120	
Db	59 VALAIAHRIIESERCYSGILVALASNLYSERISPSERVEVILLEGILNEULEASN	78	
QY	121 CCCAACAGCGACACATTATTTCAGGACCTTCAGGCCCTTGAAGCACAGGATTCAG	180	
Db	79 PROASNAARGILTHRIETYPHEARGPSPEARGPVLEULYSASPSERARPHGELN	98	
QY	181 TTGCGAATTTTTCAGCAGTGAAGCTCAAAATATCATTTGCAAAAGCTCAATTCGAT	240	
Db	99 LEULEASNPHERSERISERGLNEULYSVALSERLEUTHRASVALSERILIESERASP	118	
QY	241 GAAGAAATATCTTTGGCCAGCTCTATACGATGCCCCACAGAAAGTTACACCACTATC	300	
Db	119 GLUGIATGYTRPHECYSGILNEUTYRTHRSPPROGILGILUSERYTRTHRIE	138	
QY	301 ACAGTCTGGTCCACACAGCTAATCTGATGATATCCAGAAAGACACTGCGGTGAA	360	
Db	139 THRVALLEUVALPROPROARGASNEUHEPHERILIESPILGILNYSAPRTHALAVAGLU	158	
QY	361 GGTGGAGATTGAAGTAACTGACAGCTGATNGGCCAGCAAGCCAGCCAGCATATCAGG	420	
Db	159 GLUGILGILILEGLILVALASNCYSTRHALAMELALSERLSPROALATHTHRIEARG	178	
QY	421 TGGTTCAGAGGGAACACACAGACTAAAGGCNAATCGGAGGCGAAGAGTGGTGCAGATG	480	
Db	179 TRPHEULYSGLIYASRTHGILNEULYSGLIYLSERSELVALIGLIGLUTTPSERASMET	198	
QY	481 TACACTGTGACCACTGACCTGATGCTGAAGGTGACAGGACGATGGGGTCCAGTG	540	
Db	199 TYRTHRVALTHPSERGLNEUHEPHERILIESPILGILNYSAPRTHALAVAGLU	218	
QY	541 ATCTGCCAGGTGGAGACACCCCTGGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAA	600	
Db	219 IIECYSGILVALIGLILHSPROALAVALTHRIDLYASNEUGINTHTGILAAGYTRYLEGLU	238	
QY	601 GTACAGTTAAGCCCTCAAGTGCACATTCAGATGACTTATGCTCTACAGGCTTAACCCGG	660	
Db	239 VALGINTYRLSPROGILNVALHISILLEGIMETHRYTRPHEULGILNEULTHIRAY	258	
QY	661 GAAGGGGACGGCGTTGAAGTTAACATGTGAAGCCATCGGGAAGCCCGACGCTGTGATGTA	720	
Db	259 GLUGILYASPRALALEUGILNEUTHCYSGILUALILEGLIYLSPROGILNPROVALMEVEL	278	
QY	721 ACTTGGGTGAGATGTCATGATGAATCCCTCACAGCCGCTACTGCTGGGCCCAACTG	780	
Db	279 THRTRVALARGVALASPAISPGILMETPROGILNHSIALAVALLEUSERGLYPROASNEU	298	
QY	781 TTCATCATATACCTTAACCAAAACAGATAATGTGATACATACCGCGTGTGAAGTTCAACATA	840	
Db	299 IIEIIEHSNANLEUASNLYSTHASPASGLYTHRYTRARGCYSGILUALISERASNILE	318	
QY	841 GTGGGGAAGAGCTCACTCGGATTAATATCTGTATGTATACGATCCCCCACACATATCCCT	900	

Db	319	VALCIGYLSALAHISSErAsPTyrmEtLeUtyrValtyrAsProthrThrIlePro	338
Qy	901	CGTCCGACAACACACACACACACACACACACACACACACACATCCTTACATCATC	960
Db	339	ProthrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleuThrIleIle	358
Qy	961	ACAGATTCCGACGACGTGAAGAGAGCTGCATCAGCGCATGTGCATCAT	1008
Db	359	ThrAspSerArGAlaCIgUGIUGIUGISerIleArGAlaValAspHis	374
RESULT 6			
AAV94341			
ID	AAV94341 standard; Protein: 442 AA.		
XX			
AC	AAV94341;		
XX			
DT	22-AUG-2000 (first entry)		
XX			
DE	Human cell surface receptor protein #8.		
XX			
KW	Human: HCSRp; cytosolic; antiarthritic; antiinflammatory; antistomatitic; immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia; Alzheimer's diseases; multiple sclerosis; epilepsy.		
KW			
KM			
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..44	
FT		/label= Signal_peptide	
FT	Protein	45..442	
FT		/label= HCSRp-8	
FT	Domain	57..126	
FT		/label= Immunoglobulin_domain	
FT	Domain	159..222	
FT		/label= Immunoglobulin_domain	
FT	Domain	260..315	
FT		/label= Immunoglobulin_domain	
FT	Domain	375..394	
FT		/label= Transmembrane_domain	
FT	Region	53	
FT		/note= "potential phosphorylation site"	
FT	Region	67	
FT		/note= "potential glycosylation site"	
FT	Region	101	
FT		/note= "potential glycosylation site"	
FT	Region	103	
FT		/note= "potential phosphorylation site"	
FT	Region	113	
FT		/note= "potential glycosylation site"	
FT	Region	115	
FT		/note= "potential phosphorylation site"	
FT	Region	155	
FT		/note= "potential phosphorylation site"	
FT	Region	165	
FT		/note= "potential glycosylation site"	
FT	Region	176	
FT		/note= "potential phosphorylation site"	
FT	Region	190	
FT		/note= "potential phosphorylation site"	
FT	Region	233	
FT		/note= "potential phosphorylation site"	
FT	Region	241	
FT		/note= "potential phosphorylation site"	
FT	Region	304	
FT		/note= "potential glycosylation site"	
FT	Region	308	
FT		/note= "potential glycosylation site"	
FT	Region	310	
FT		/note= "potential phosphorylation site"	
FT	Region	329	
FT		/note= "potential phosphorylation site"	

FT	Region	/note= "potential phosphorylation site"
FT	368	/note= "potential phosphorylation site"
FT	Region	432
FT		/note= "potential glycosylation site"
XX		
PN	W0200028032-A2.	
XX		
PD	18-MAY-2000.	
XX		
PE	12-NOV-1999;	99W0-US26742.
XX		
PR	12-NOV-1998;	98US-0191280.
PR	07-DEC-1998;	98US-0206647.
PR	08-MAR-1999;	99US-0123404.
XX		
PA	(INCY-) INCYTE PHARM INC.	
XX		
PI	Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;	
PI	Hillman JL, Bandman O, Azimzal Y, Au-Young J;	
XX		
DR	WPI: 2000-376546/32.	
DR	N-PSDB: AAA27051.	
XX		
PT	New human cell surface receptor protein and polynucleotide useful for	
PT	diagnosis, prevention and treatment of cancer, immune disorders,	
PT	infection and neuronal disorders	
XX		
PS	Claim 1; Page 81-82; 97pp; English.	
XX		
XX	The present sequence is a novel human cell surface receptor protein	
CC	(HCSR) designated HCSR-8. The nucleotide sequence was identified in	
CC	Incyte Clone 312256 from the cDNA library LUNCN0702, which was made from	
CC	RNA isolated from lung tissue. A number of Incyte Clones were used to	
CC	assemble the consensus sequence. BLAST analysis showed that the sequence	
CC	is homologous to Immun-superfamily protein B12 g3779242. HCSR and its	
CC	antagonist are useful for preventing or treating disorders associated	
CC	with decreased or increased expression or activity of HCSR. Such	
CC	disorders include cancers such as leukemia and melanoma, immune	
CC	disorders such as rheumatoid arthritis, asthma and atherosclerosis,	
CC	bacterial and parasitic infections and neuronal disorders such as	
CC	akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.	
CC	Polynucleotides encoding HCSRs may be used as hybridisation probes to	
CC	diagnose these conditions. Anti-HCSR antibodies may be used as	
CC	antagonists, as a targeting or delivery mechanism for bringing	
CC	pharmaceutical agents into contact with cells or tissues expressing	
CC	HCSR and for diagnosis of HCSR-related disorders. HCSR and its	
CC	catalytic or immunogenic fragments are useful for drug screening using	
CC	libraries of compounds.	
XX		
SO	Sequence	442 AA;
Alignment Scores:		
Pred. No.:	7.82e-151	Length: 442
Score:	1761.00	Matches: 336
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	97.78%	Indels: 0
DB:	21	Gaps: 0
US-09-778-187B-1.COPY_130_1137 (1-1008) x AAY94341 (1-442)		
QY	1 ATCCCCACAGGAGGAGGACAGAACTGTTTACGAAAGACGTGACAGTGCAGGAGAG	60
DB	39 IIEPOTTHGIVASPGILGInshnshneuhethrIVASpValTHnValIIeGInGILyGIn	58
QY	61 GTTGGACCATCAGTGGCAAGTCAATTAAGAGTGACGACTCTGTGATTCACACTGAA	120
DB	59 VALAIAHrIIeserCYsgCInValAsnIshysersAspserValIIeGInLeuAsn	78
QY	121 CCCAACAGGACACATTTATTTACAGGAGCTTCAGCCCTTTGAAGACAGACAGCTTTCAG	180
DB	79 PRAshATVgInTHrIIeETyrPheArVgAspPheArGpPoleuLVASpSerArGpPheGIn	98

QY 181 TTGCTGAATTTTCTTACAGTGAACCTCAAGTATCATTTGACAAACGCTCAATTTCTGAT 240
 |||||||
 Db 99 LeuLeuSnPhSeSerSerSerGluLeuLysValSerLeuThrAnValSerLleSerasp 118
 QY 241 GAAGGAAGATACCTTTTGCCAGCTCTATACGATCCCCACAGAAAGTTACACCAATC 300
 |||||||
 Db 119 GluLlYArtyrPhcysGlnLeuTyThrAspProGlnGlnSerTyThrThlle 138
 QY 301 ACACTGCTGGCCACACAGCTAATCTGATGATATCCGAAGAAGACACTGCGGTGAA 360
 |||||||
 Db 139 ThrValLeuValProProAlaGlnLeuMetLleaspLleGlnLysAspThrAlaValGlu 158
 QY 361 GGTGAGAGATTTGAAGTCAACTGCACTGATAGCCACAGCAAGCCACGACATCATCAGG 420
 |||||||
 Db 159 GlyGluGluLleGluValAsnCysThrAlaMetAlaSerLysProAlaThrThlLeArg 178
 QY 421 TGTGTTCAAAGGGAACACAGAGCTAAAAGGCAATCGGAGTGGGAAGAGTGCTCAGACATG 480
 |||||||
 Db 179 TrpPheLysGlnAnThrGlnLeuLysGlyLysSerGluValGluGluTTPSerAspMet 198
 QY 481 TACACTGTGACAGTCACTGATGCTGAGTGCACAAAGGAGAGAGATGGGGTCCAGTG 540
 |||||||
 Db 199 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspAspGlyValProVal 218
 QY 541 ATCTGCCAGGTGAGACACCTGCGGTCACTGGAACCTGCAGACCCAGCGGTATCTAGAA 600
 |||||||
 Db 219 IleCysGlnValGlnHisProAlaValThrGlyAsnLeuGlnThrGlnArgTyLeuGlu 238
 QY 601 CTACAGTATAAGCTCTCAAGTGCACATTCAGATGACTTATCTCTACAAAGCTTAAACCCG 660
 |||||||
 Db 239 ValGlnTyrrysProGlnValHisLleGlnMetThrTyrrProLeuGlnGlyLeuThrArg 258
 QY 661 GAAGGGAGCGGCTTGAGTTAACATGTGAAGCCATCGGGAAGCCCGCGGTGATGTA 720
 |||||||
 Db 259 GluLlYAspAlaLeuGlnLeuThrCysGlnAlaLleGlyLysProGlnProValMetVal 278
 QY 721 ACTTGGTGAAGTGCATGATGAATGCTCAACACGCCCTACTGCTGGGCCCAACCTG 780
 |||||||
 Db 279 ThrTyrrAlaArgValAspAspGlnMetProGlnHisAlaValLeuSerGlyProAsnLeu 298
 QY 781 TTTCATCAATACCTAAACAAACAGATATGTCATACCGCTGTGAAGCTTCAACATA 840
 |||||||
 Db 299 PheLleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrrArgCysGlnAlaSerAsnLle 318
 QY 841 GTGGGGAAGCTCACTGCGATTATATGCTGATGATATACGATCCGCCCAACATCCCT 900
 |||||||
 Db 319 ValGlyLysAlaHisSerAspTyrrMetLeuTyValTyrrAspProThrThrLlePro 338
 QY 901 CTTCCCAACAACACACACCACACACACACACACACACACATCTTACCATCATC 960
 |||||||
 Db 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 358
 QY 961 ACAGATCCCGAGCAGGTGAAAGGCTCGATCAGGCGACATGATCAT 1008
 |||||||
 Db 359 ThrAspSerArgAlaGlyGluGlnGlySerLleArgAlaValAspHis 374

RESULT 7
 AAY45092
 ID AAY45092 standard: Protein; 442 AA.
 AC AAY45092;
 XX
 DT 31-MAY-2000 (first entry)
 XX
 DE Human lymphoid derived dendritic cell adhesion molecule.
 XX
 KW Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
 KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
 KW biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.
 XX

OS Homo sapiens.
 XX
 FH Key
 FT Domain
 FT Peptide
 FT Protein
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Domain
 FT Domain
 FT Domain
 FT Domain
 PD 17-FEB-2000.
 PD 05-AUG-1999; 99MO-US17905.
 PR 07-AUG-1998; 98US-0095672.
 XX (IMMUNEX CORP.
 PA Baum PR, Fanslow WC;
 XX WPI; 2000-205712/18.
 DR N-PSDB; AA250882.
 XX
 PT Novel molecules designated LDCAM are capable of altering or modulating
 PT T cell function -
 XX
 PS Claim 7; Page 42-43; 44pp: English.
 XX
 CC The present amino acid sequence is the human lymphoid derived dendritic
 CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
 CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
 CC region of B7-1. Human LDCAM is expressed in breast, retina, foetal
 CC liver, spleen and heart, lung, muscle, placenta, thyroid and lung
 CC carcinoma. LDCAM polypeptides interacts with T cell surface molecules
 CC to alter signalling and inhibits T cell proliferation, bind to
 CC themselves and B7L-1, an LDCAM binding protein and increases natural
 CC killer (NK) cell populations. It may be used to measure the biological
 CC activity and as quality control reagents of LDCAM binding proteins.
 CC LDCAM may be used for treating disorders associated with malfunctioning
 CC of immune system, inflammation, autoimmune disorders, viral infected
 CC cells, infectious diseases and for killing tumour cells. They are also
 CC useful for prevention or reducing the effect of organ and bone marrow
 CC transplant rejection and for modulating T cell immune responses. LDCAM
 CC polypeptides may also be used as carriers for delivering agents attached
 CC to T cells or cells bearing B7L-1.
 CC
 XX
 SO Sequence 442 AA:
 Alignment Scores:
 Pred. No.: 7,82e-151 Length: 442
 Score: 1761.00 Matches: 336
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.78% Indels: 0
 DB: 21 Gaps: 0

```

US-09-778-187b-1_COPY_130_1137 (1-1008) x AAY45092 (1-442)
OY 1 ATCCCAAGAGTGGAGATCTGTTACGAAGACGTGACAGTATCGAGGAG 60
DB 39 IIEPRTGCLYSPRLYGLNLSNLEUPHETHLYASPAVLAITHRVALLIEGLNGLYGLN 58
OY 61 GTTGCAGCATCATGTTGCCAATCAATAGAGTACAGTCTGTGATTGACTGTAAT 120
DB 59 VALAIAETHRIESECYSGINVALASNLYSERAPSPERVALIIEGLNLEUASN 78
OY 121 CCCAAGCAGCAGCATTTATTTCAGGAGCTTGAGCCTTTTGAAGACAGCAGCTTTCAG 180
DB 79 PROASNAARGLINTHRIETRYRPHENARGSPRHEARGPROLEUYSAPSERAPGHEGLN 98
OY 181 TTTCGTAATTTTCTAGCAGTCAACTCAAAAGTATCATTTGCAAAAGCTTCATTTCTGAT 240
DB 99 LEULEASNPHESERSESERSEGLULEULYSVALSERLEUTHRASNVALSERIIESEASP 118
OY 241 GAAGAAGATACCTTTTGGCAGCTCTATACCGATCCCCACAGGAAGATTACACCATC 300
DB 119 GLUGLYARGTYRPHCYSGINLEUITYRTHASPRPROGLINLSERTYRTHRIIE 138
OY 301 ACAGTCTGGTCCACACAGTAACTGATGATGATATCCAGAAAGACACTGCGGTGGAA 360
DB 139 THVALLEUVALPRPROBARGASNLEUMETLEASPIIEGLNLYSAPTHRALVALGLU 158
OY 361 GGTGAGAGATTGAGTCAACTGCTGATGGCCAGCAAGGACAGCAGTATCAGG 420
DB 159 GLYGLUGLUIIEGLNVALASNCTHRIALMETALASERTYSPROALATHRIIEARG 178
OY 421 TGGTTCAAGGGAACACAGAGCTAAAGGCAATCGAGGTGAGAGAGTGTGACATG 480
DB 179 TRPHELYSGLYASNTHRGILEULYSGLYLSERGLIUALGLUINTRPSEASP 198
OY 481 TACACTGTACACGTCAGTGCATGAGGTGCACAGAAGAGACGATGGGTCACAGT 540
DB 199 TYRTHVALTHSERGLNLEUMETLEULYSVALNLSLYSPASPRGLYVALPROVAL 218
OY 541 ATCTCCAGGTGAGACACCTCGCGTCACTGGAACCTGAGACACAGCGGTATCAGAA 600
DB 219 IIECYGLNVALICLUNHSPROALVALTHRCLYASNLEUGLINTHRIINAGTYRLEGLN 238
OY 601 GTACAGTATAGCCTCAAGTCACTCAATGATGATGATGATGATGATGATGATGAT 660
DB 239 VALGLINTYRSPROGLINVALNLSIIEGLNMETHTYRPROLEUGLINCILYLEUTHARG 258
OY 661 GAAGGAGCGCGTGTGATTAACATGTAAGCAATCGGGAAGGCCAGCCTGTGATGTA 720
DB 259 GLUGLYASPRALASLEUGLIUEUTHRCYSGIUALAIEGLYLSYSPROGLINPROVALMETVAL 278
OY 721 ACTTGGGTGAGATCGATGATGAATGCCTCAACACGCGCTACTGTCTGGGCCAAGCTG 780
DB 279 THRTTRVALARGVALASPRASPRGLIMETPROGLINHIALVALLEUBERGILYPROASNLEU 298
OY 781 TTTCATCAATTAACSTAACAACAGATATGATGATACCCGCTGTGAAGCTTAACAATA 840
DB 299 PHEILASNASNLEUASNLYSTHASPASNGLYRTHYRARGYSGIUALASERASIIIE 318
OY 841 GTGGGGAAGCTGATCGGATTTATATGCTGATGATGATGATGATGATGATGATGAT 900
DB 319 VALGLYVALAHNLSERAPRYRMELEUTHYRVALITYRSPROPROTHRIITHRIIEPRO 338
OY 901 CCTCCCAACAACAACACACACACACACACACACACACACACACACATCTTACATCATC 960
DB 339 PROPRDTHTRHTRHTRHTRHTRHTRHTRHTRHTRHTRHTRHTRHTRHTRHTRHTR 358
OY 961 ACAGATTCGGCAGCAGTGAAGAAGCTGATGAGGCACTGATCAT 1008
DB 359 THASPSERARGALISGLYGLNGLYSERILEARGALVALASPRIS 374

```

RESULT 8
AAE19887

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ID AAE19887 standard; Protein: 442 AA.
XX
AC AAE19887;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
XX
KW Human: hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KW liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN W0200214557-A1.
XX
PD 21-FEB-2002.
XX
PE 15-AUG-2001; 2001WO-US25690.
XX
PR 15-AUG-2000; 2000US-225264P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Reeves RH, Yoshinori M;
XX
DR WPI; 2002-241913/29.
XX
PT Detecting cell proliferative disorder associated with tumor suppressor
PT lung cancer (TSLC) 1 in subject, comprises contacting proliferating
PT cell of subject with reagent detecting TSLC1 and detecting modification
PT in TSLC1 level
XX
PS Disclosure: Page 49-50; 59pp; English.
XX
CC The invention relates to a method for detecting cell proliferative
CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a
CC subject. The method comprising contacting a cell component of a
CC proliferating cell with a reagent that detects level of the cell
CC component in the proliferating cell and determining modification in the
CC level of the cell component in proliferating cell as compared with a
CC healthy cell, where modification indicates disorder associated with a
CC TSLC1. The method is useful for detecting a cell proliferative disorder
CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
CC therapy and for treating a cell proliferative disorder such as lung
CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
CC carcinoma) or pancreatic cancer associated with modification of TSLC1
CC production, where a reagent which modulates (preferably, increases) TSLC1
CC level in the cells, is employed. The present sequence is human TSLC1.
XX
SQ Sequence 442 AA;
XX
Alignment Scores:
Pred. No.: 7,82e-151
Score: 1761.00 Length: 442
Percent Similarity: 100.00% Matches: 336
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 23 Gaps: 0

```

```

US-09-778-187b-1_COPY_130_1137 (1-1008) x AAE19887 (1-442)
OY 1 ATCCCAAGAGTGGAGATCTGTTACGAAGACGTGACAGTATCGAGGAG 60
DB 39 IIEPRTGCLYSPRLYGLNLSNLEUPHETHLYASPAVLAITHRVALLIEGLNGLYGLN 58
OY 61 GTTGCAGCATCATGTTGCCAATCAATAGAGTACAGTCTGTGATTGACTGTAAT 120
DB 59 VALAIAETHRIESECYSGINVALASNLYSERAPSPERVALIIEGLNLEUASN 78
OY 121 CCCAAGCAGCAGCATTTATTTCAGGAGCTTGAGCCTTTTGAAGACAGCAGCTTTCAG 180

```

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Db 79 ProAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 98
QY 181 TTGCTGAATTTTCTAGCAGTGAAGTCAATGATCATGAGCAACGCTCATTTCTGAT 240
Db 99 LeuLeuAsnProSerSerSerGlnLeuLysValSerLeuThrAsnValSerIleSerAsp 118
QY 241 GAAGGAAGATACTTTTGGCAGCTCTATACCGATCCGCCACAGAAAGTTACACCAATC 300
Db 119 GluGlnArgTyrPheCysGlnLeuTyrThrAspProGlnGlnLysSerTyrThrIle 138
QY 301 ACAGTCCCGGTCCACCAACCTAATCTGATGATCATATCCGAAAGACACTCCGCTGAA 360
Db 139 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 158
QY 361 GGTAGAGAGATTGAAGTCAACTGCACCTGCTATGGCAGACCAAGCCAGCAGCATATCAG 420
Db 159 GlyGlnGlnIleGlnValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg 178
QY 421 TGGTTCAAAGGGAACACAGAGAGCTAAAGCAATCGAGGTGGAAGAGTGGTCAAGATG 480
Db 179 TrpPheLysGlnAsnThrGlnLeuLysGlyLysSerGlnValGlnGlnIleTrpSerAspMet 198
QY 481 TACACTGGACCACTCAAGCTGATGCTGAGGTGCACAAAGAGAGCATGGGGTCCAGCTG 540
Db 199 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspAspGlyValProVal 218
QY 541 ATCTGCCAGGTGAGACACCCCTGCGTCACTGGAACCTGCAGACCCGCGCTATCTGAA 600
Db 219 IleCysGlnValGlnHisProAlaValThrGlnLysnLeuGlnThrGlnArgTyrLeuGln 238
QY 601 GTACAGTAATAAGCTCAAGTGCACATTCAGATGACTTATCCTTACAAGGCTTAACCCGG 660
Db 239 ValGlnTyrLysProGlnValHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 258
QY 661 GAAGGGAGCGGGCTTGAGTTAATCATGTGAAGCCATCGGGAAGCCCGACCTGATGTA 720
Db 259 GlnGlnLysPalaLeuGlnLeuThrCysGlnAlaIleGlnLysProGlnProValMetVal 278
QY 721 ACTTGGGTGAGAGTGCATGATGAATGCTCAACACAGCCGACTGTCGGGCCCAACCTG 780
Db 279 ThrThrValArgValAspAspGlnMetProGlnHisAlaValLeuSerGlyProAsnLeu 298
QY 781 TTCTCATTAATACCTAAACAACAGATATGATACATACCGCTGTGAAGCTTCAACATA 840
Db 299 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 318
QY 841 GTGGGGAAGCTCAGTGGGATTATAGCTGATGATATACATATCCGCCACAACTATCCCT 900
Db 319 ValGlnLysAlaHisSerAspTyrMetLeuTyrValTyrAspProProThrThrIlePro 338
QY 901 CTTCCCAACAACACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAATC 960
Db 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 358
QY 961 ACAGATCCCGCAGCAGTGAAGAAGCTGCATCAGGCGCAGTGCATCATC 1008
Db 359 ThrAspSerArgAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 374

```

RESULT 9

AAV45093

ID AAV45093 standard; Protein; 423 AA.

AC AAV45093;

XX 31-MAY-2000 (first entry)

DE Mouse lymphoid derived dendritic cell adhesion molecule.

KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;

KW biological activity; quality control reagent; treatment; inflammation;

KW immune system disorder; autoimmune; viral infection; infectious disease;

KW organ transplant rejection; bone marrow; modulator; immune response.

```

XX OS Mus sp.
FH key Location/Qualifiers
FT Domain 1..356
FT Modified-site /label= Extracellular_domain
FT Modified-site 49..51
FT Modified-site /note= "N-Glycosylation site"
FT Modified-site 83..85
FT Modified-site /note= "N-Glycosylation site"
FT Modified-site 95..97
FT Modified-site /note= "N-Glycosylation site"
FT Modified-site 147..149
FT Modified-site /note= "N-Glycosylation site"
FT Modified-site 286..288
FT Modified-site /note= "N-Glycosylation site"
FT Modified-site 290..292
FT Modified-site /note= "N-Glycosylation site"
FT Domain 357..377
FT Domain /label= Transmembrane_domain
FT Domain 378..423
FT Domain /label= Cytoplasmic_domain

XX PN WO200008158-A2.
XX PD 17-FEB-2000.
XX PE 05-AUG-1999; 99NO-US17905.
XX PR 07-AUG-1998; 98US-0095672.
XX PA (IMMUNEX CORP.
XX PI Baum PR, Fanslow WC;
XX DR WPI; 2000-205712/18.
XX DR N-PSDB; AA250883.
XX PT Novel molecules designated LDCAM are capable of altering or modulating
XX T cell function
XX PS Claim 7; Page 46-47; 44pp; English.
XX CC The present amino acid sequence is the mouse lymphoid derived dendritic
XX CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
XX CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
XX CC region of B7-1. Mouse LDCAM is found on whole embryo, testes, triple
XX CC negative cells murine splenic and lymph node CD8+, S49.1 and dendritic
XX CC cells. LDCAM polypeptides interacts with T cell surface molecules
XX CC to alter signalling and inhibits T cell proliferation, bind to
XX CC themselves and B7-1, an LDCAM binding protein and increases natural
XX CC killer (NK) cell populations. It may be used to measure the biological
XX CC activity and as quality control reagents of LDCAM binding proteins.
XX CC LDCAM may be used for treating disorders associated with malfunctioning
XX CC of immune system, inflammation, autoimmune disorders, viral infected
XX CC cells, infectious diseases and for killing tumour cells. They are also
XX CC useful for prevention or reducing the effect of organ and bone marrow
XX CC transplant rejection and for modulating T cell immune responses. LDCAM
XX CC polypeptides may also be used as carriers for delivering agents attached
XX CC to T cells or cells bearing B7-1.
XX SQ Sequence 423 AA;

```

Alignment Scores:

```

Pred. No.: 4.99e-149 Length: 423
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.67% Indels: 0
DB: 21 Gaps: 0

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US-09-778-187B-1_COPY_130_1137 (1-1008) x AAV45093 (1-423)


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OY 1 ATCCCCAGAGTGATGGCAGAACTGTTTACGAAGAGCTGACGATCGAGGAGAG 60
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    |||
DB 21 IIEPCTHGLYAspELyGlnAsnLeuPheThrLyAspValThrValIleGluGlyGln 40
    |||
    |||
    |||
OY 61 GTTGGACCATCTGTCAGCATTAAGAGGACGATCTGTGATTGACGACTGAT 120
    |||
    |||
    |||
DB 41 ValAlaThrIleSerCysGlnValAsnLysSerAspAspSerValIleGlnLeuLeuAsn 60
    |||
    |||
    |||
OY 121 CCCAACAGGACAGACATTTATTTACAGGACTTCAGCCCTTTGAAGAGCAGAGTTTCA 180
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    |||
    |||
DB 61 ProAsnArgGlnThrIleLysrPheArgAspPheArgProLeuLysAspSerArgPheGln 80
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    |||
    |||
OY 181 TTGCTGAATTTTCTAGCAGTAACTCAAGATATCATTAAGCAAAAGCTGTCAATTCTGAT 240
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    |||
DB 81 LeuLeuAsnPheSerSerSerGluLeuLysValSerLeuThrAsnValSerIleSerAsp 100
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    |||
OY 241 GAAGGAAGATACTTTTGGCAGCTCTATACCGATCCCGCCAGGAAGTTACACGACATC 300
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DB 101 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 120
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OY 301 ACAGTCCCTGGTCCACACAGATATCTGATGATGATATCCAGAAAGACACTCGCGTGAA 360
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    |||
DB 121 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 140
    |||
    |||
    |||
OY 361 GGTGAGAGATTTGAGTCACTGCTATGCGCCAGCAAGCCACGACTATCAGG 420
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    |||
DB 141 GlyGluGlnIleGluValAsnLysThrAlaMetAlaSerLysProAlaThrThrIleArg 160
    |||
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    |||
OY 421 TGGTTCAAGGGACACACAGCTAAAGGCAATCGGAGGTGGAAGAGTGTTCAGCATG 480
    |||
    |||
    |||
DB 161 TTPPheLysGluValAsnLysLysLysGlyLysSerGluValGluLysTPSerAspMet 180
    |||
    |||
    |||
OY 481 TACACTGTACACAGTGTGATGCTGTAAGAGTGCACACAGAGAGAGGAGGAGGCTCCAGTG 540
    |||
    |||
    |||
DB 181 TyrThrValThrSerGlnLeuMetLysValHisLysGlnAspArgValProVal 200
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    |||
    |||
OY 541 ATCTGCCAGGTGAGAGACCCCTCGGCTACTGGAACCTGCAGACCCGCGATATAGAA 600
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    |||
DB 201 TLeCysGlnValGlnThrProAlaValThrGlyAsnLeuGlnThrGlnArgTyrLeuGln 220
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    |||
    |||
OY 601 GTACAGTATTAAGGCTCAATGACATGATGATGATGATGATGATGATGATGATGATGATG 660
    |||
    |||
    |||
DB 221 ValGlnTyrLysProGlnValHisIleGlnMetCysThrTyrProLeuGlnGlyLeuThrArg 240
    |||
    |||
    |||
OY 661 GAAGGAGAGCCCTGATTAACATGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
    |||
    |||
    |||
DB 241 GluGlyAspAlaPheGlnLeuThrCysGlnAlaIleGlyLysProGlnProValMetVal 260
    |||
    |||
    |||
OY 721 ACTTGGGTAGAGTSGATGATGAATGCTCTCAACAGCCGCTACTGTCTGGCCCAACCTG 780
    |||
    |||
    |||
DB 261 ThrThrValArgValAspArgGlnMetProGlnHisAlaValIleuSerGlyProAsnLeu 280
    |||
    |||
    |||
OY 781 TTCATCAATTAACCTAAACAAACAGATATGATGATGATGATGATGATGATGATGATGAT 840
    |||
    |||
    |||
DB 281 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgGlyGlnAlaSerAsnIle 300
    |||
    |||
    |||
OY 841 GTGGGGAAGGCTCACTCGGATTTATGCTGATGATGATGATGATGATGATGATGATGATG 900
    |||
    |||
    |||
DB 301 ValGlyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProThrThrIlePro 320
    |||
    |||
    |||
OY 901 CCTCCCAACAACAACACACACACACACACACACACACACACACATCTTACATCATC 960
    |||
    |||
    |||
DB 321 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 340
    |||
    |||
    |||
OY 961 ACAGATTTCCGAGCAGAGTGAAGAAGCTCGATCAGGAGGAGTGAATAT 1008
    |||
    |||
    |||
DB 341 ThrAspSerArgAlaGlyGluGlnGlyThrIleGlyAlaValAspHis 356
    |||
    |||
    |||
RESULT 10
AAB25586
ID AAB25586 standard; Protein; 364 AA.
XX
AC AAB25586;

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```

XX 21-NOV-2000 (first entry)
DT Protein encoded by human secreted protein gene #11.
XX
XX
XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antineumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; valnery; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human.
XX
XX Homo sapiens.
XX
XX WO200029435-A1.
XX
XX 25-MAY-2000.
XX
XX 27-OCT-1999; 99WO-US25031.
XX
XX 28-OCT-1998; 98US-0105971.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX NI J, Ruben SM, Olsen HS, Young PE, Kenny JD, Moore PA, Wei Y;
XX Greene JM;
XX
XX WPI: 2000-387742/33.
XX
XX N-PSDB: AAB0616.
XX
XX Isolated nucleic acid molecules encoding human secreted proteins are
XX used for the prevention, amelioration and treatment of autoimmune,
XX inflammatory, hyperproliferative and cardiovascular disorders, cancer,
XX wounds, and infectious diseases -
XX
XX Claim 1; Figure 28A-B; 803bp; English.
XX
XX PS
XX
XX The present invention relates to 12 secreted human proteins and the
XX nucleotide sequences encoding them. The polynucleotide sequences given in
XX in AAB0606-A80623 encode the 12 secreted protein sequences given in
XX AAB25576-B25593. The human secreted proteins have various activities
XX dependent on the tissues in which they are expressed. Examples of the
XX activities of the proteins include: immunosuppressant;
XX anti-inflammatory; antirheumatic; antineumatic; dermatological;
XX antiproliferative; antiarteriosclerotic; anticancer; valnery;
XX antiviral; antibacterial; and antifungal activity. The proteins,
XX polypeptides, agonists and antagonists may be used to treat prevent
XX and/or diagnose various diseases, disorders and conditions examples of
XX which include: immune disorders e.g. Addison's disease, rheumatoid
XX arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
XX e.g. inflammatory bowel disease, Crohn's disease and nephritis;
XX hyperproliferative disorders such as paraproctelasma and purpura;
XX cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
XX cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
XX sequences may also be used in wound healing and the treatment of
XX infectious diseases. The human secreted protein gene #11 and protein
XX sequences are represented in sequences AAB0616 and AAB25586. Sequences
XX AAB0677-A80682 represent genes related to the secreted protein gene#11.
XX
XX
SQ Sequence 364 AA:

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Alignment Scores:

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Pred. No.: 1 07e-145 Length: 364
Score: 1704.00 Matches: 325
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.61% Indels: 0
DB: 21 Gaps: 0

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US-09-778-187B-1_COPY_130_1137 (1-1008) x AAB25586 (1-364)

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QY 1 ATCCACAGGTGATGGGAGAAATCTTTTACGAAGAAGCTGACATGATCAGGAGAG 60
Db 11EProthrglyaspGlylnasnleuPhehrlyaspValThrVal11leGlnGlylu 58
QY 61 GTTCGACCATCATTTGGCAGATCAATPAGAGTGACGACTGTGGATTCCACTGAT 120
Db 59 ValAthrIleSerCysGlnValasnlySeraspSerVal11leGlnleuasn 78
QY 121 CCCAAGAGGACGACATTTATTTGAGGACTTCAGGCTTTCGAAGGAGCAGGTTTCAG 180
Db 79 ProasnArglnThrIleTyrPheArgaspPheArgProleuLysaspSerArgPheGln 98
QY 181 TTGCTGAATTTTTCAGCAGTGAATCAAGATTCATTTGACAAACGCTCAATTTCTGAT 240
Db 99 LeuLeuasnPheSerSerSerGlnleuLysValSerleuThrAsnValSerIleSerasp 118
QY 241 GAAGGAGATCTTTTGGCAGCTCTATACCATTCCTCCACAGGAAAGTTACACCATC 300
Db 119 GlnGlyArgTyrPheCysGlnleuTyrThrAspProGlnGlnSerTyrThrIle 138
QY 301 ACACTCTGGTCCACACGTAATCTGATGATGATATCCGAAGAAGACACTGGGTTGAA 360
Db 139 ThrValleuValProProArgasnleuMetIleaspIleGlnLysaspThrAlaValGln 158
QY 361 GGTGAGAGATTTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACTATCAGG 420
Db 159 GlyGlnGlnIleGlnValasnCysThrAlaMetAlaSerLysProAlaThrThrIleArg 178
QY 421 TGGTTCAAGGAGACACAGAGCTAAAGGCAATCGAGAGTGGAAAGTGTCTACAGATG 480
Db 179 TrpPheLysGlnAsnThrGlnleuLysGlyLysSerGlnValGlnGlnTrpSerAspMet 198
QY 481 TACACTGTGACACATGACGTGATGCTGAAGGTGCACAAAGAGAGAGAGTGGGCTCCAGTG 540
Db 199 TyrThrValThrSerGlnleuMetleuLysValHisLysGlnAspArgGlyValProVal 218
QY 541 ATCTCCAGGTGAGACACCTCGGTCAGTGAAGAACTGCAGACCCAGCGGTATCTGAA 600
Db 219 IleCysGlnValGlnHisProAlaValThrGlnLysAsnleuGlnThrGlnArgTyrLeuGln 238
QY 601 GTACAGTATAGCTCCTAAGTGCACATTCAGATGACTATCTCTACAAAGGCTTAACCCGG 660
Db 239 ValGlnTyrLysProGlnValHisIleGlnMetThrTyrProleuGlnGlyLeuThrArg 258
QY 661 GAAGGGAGCCGCTTGAAGTAAACATGTGAAGCCATCGGAAGCCCAAGCCGTGATGTA 720
Db 259 GlnGlyAspAlaLeuGlnleuThrCysGlnAlaIleGlyLysProGlnProValMetVal 278
QY 721 ACTTGGGTGAGAGTCCATGATGAATCCCTACACGCCGCTACTGTCTGGGCCACCTG 780
Db 279 ThrThrValArgValAspArgGlnMetProGlnHisAlaValleuSerGlyProAsnleu 298
QY 781 TTGATCAATAGCTAAACAAACAGATGAATGATACATACCGCTGTAAGCTTCAACATA 840
Db 299 PheIleAsnAsnleuAsnLysThrAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 318
QY 841 GTGGGGAAGCTCACTGGAATTATGCTGATATGATATAGATCCCCACAACTATCCCT 900
Db 319 ValGlyLysAlaHisSerAspTyrMetleuTyrValTyrAspProThrThrIlePro 338
QY 901 CCTCCCAACAACACACACACACACACACACACACACACACACACACATCATTACATC 960
Db 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrIleLeuThrIleIle 358
QY 961 ACAGATTCGCGAGCA 975
Db 359 ThrAspSerArgAla 363

```

RESULT 11
 AAB88427
 ID AAB88427 standard; protein; 443 AA.
 XX
 AC AAB88427;

XX 23-MAY-2001 (first entry)
 DT Human membrane or secretory protein clone PSEC0200.
 XX
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes.
 XX
 OS Homo sapiens.
 XX
 PN EPI067182-A2.
 XX
 PD 10-JAN-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PT Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 PS Claim 1; SEQ ID 222; 609pp + CD ROM; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantify the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
 CC (ELISA). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.
 XX
 SQ Sequence 443 AA:

Alignment Scores:
 Pred. No.: 2.16e-137 Length: 443
 Score: 1612.50 Matches: 312
 Percent Similarity: 93.77% Conservative: 4
 Best Local Similarity: 92.58% Mismatches: 20
 Query Match: 89.53% Indels: 1
 DB: 22 Gaps: 1

US-09-778-187B-1_COPY_130_1137 (1-1008) x AAB88427 (1-443)

```

QY 1 ATCCACAGGTGATGGGAGAAATCTTTTACGAAGAAGCTGACATGATCAGGAGAG 60
Db 39 11EProthrglyaspGlylnasnleuPhehrlyaspValThrVal11leGlnGlylu 58

```

OY	61	GTGGGACCATCACTGGCCAAAGTAAATAAGATGACACACTCTGTGATTCACGTAACAT	120
Db	59	VALAATATTTILIESerCYGInValAAsnLySerAspAspSerValILeGInLeuLeuAsn	78
OY	121	CCCAACAGCGACCATATTTATTTAGGAGCACTCGAGCGCTTTGAAAGGACACAGATTTCAG	180
Db	79	ProSnaATgGInTnTrILeTYrPhaATgAspPheATgProLeuLyAspSerATgPheGIn	98
OY	181	TTTGCGAATTTTTCTAGCAGTGAACCTGAAGTATCATTTGACAAACGCTCAATTTCTGAT	240
Db	99	LeuLeuAsnPheserSerSerSerGInLeuLyValISerLeuThrsnValISerILieserAsp	118
OY	241	GAAGAGACATCTTTTGGCAGCTCTATACCGATCCCCACAGAAAGTTACACACCACATC	300
Db	119	GlUGlATgTgTyrPheCYSGInLeuTYrThAspProProGInGInSerTYrTnTrnIle	138
OY	301	ACAGCGCGGTGCCACACAGTAATCTGATGATGATGATTCAGAAAGACACTGGCGGTGAA	360
Db	139	ThrValILeuValProProLgAsnLeuMetILeAspILeGInLyAspTrnALaValGIn	158
OY	361	GGTGAGGAGATTGAAGTCAACTGCACATGCTATAGGCCACGAAGCGACGACAGCATACAG	420
Db	159	GlYGInGInLIeGInValAAsnCYrThrAlaMetnAspSerLyProAlaTnTrnILeATg	178
OY	421	TGGTTCAAAAGGAAACACAGACGTAAAGGCAATCGAGAGGTGGAAGAGTGGTCAGACATG	480
Db	179	TTrPheLySGInAsnTnTrGInLeuLyGILyAspSerGInValGInGInTnTrPserAspMet	198
OY	481	TACACTGTGACCACTCAACCTGTATCTGTAGGTGCACAAAGAGACATGGGGTCCCACTG	540
Db	199	TyTnTrnValITnTrSerGInLeuMetLeuLyAsValnILySGInAspAspGILyValProVal	218
OY	541	ATGTCCAGGTGGAGACACCCGTGGCTACTGTGGAAACCTGACAGACCCGAGCGTATCTAGAA	600
Db	219	ILeCYSGInValIGInLInSProAlaValThrGILyAsnLeuGInTnTrGInATgTYrLeuGIn	238
OY	601	GTACAGTATAAGCCTCAAGTGCACATTCAGATGACTTATCTCTACAAAGCTTAAACCCGG	660
Db	239	ValGInTYrLysProGInValnILnILeGInMetThrTYrProLeuGInGInLeuTnTrATg	258
OY	661	GAAGGGACCGCGTTGAGTTAACTGTGAAGCCATCGGGAAGCCCAAGCCTGTGATGTGA	720
Db	259	GlUGInLyAspAlaLeuGInLeuThrCYSGInValALeGILyAspProGInProValMetVal	278
OY	721	ACTGGCGGAGAGTGCATGATGAATCCCTCAACACGCGCTACTGTGGCGCCCAACCTG	780
Db	279	ThnTrPValATgValAspAspGInMetSerProGInILnILaValILeuserGILyProAsnLeu	298
OY	781	TTTCATCATTAACCTAAACAAAACAGATATGTGTACATACCGCTGTGAAGCTTCAACATGA	840
Db	299	PheILeAsnAsnLeuAsnLyThrAspAsnGILyThrTnTrATgCYSGInLAsSerAsnILe	318
OY	841	GTGGGGAAAGCTCACTCGGATTAATATGCTGTATGTATATACATCCCCCACAATATCCCT	900
Db	319	ValIGInLyValnILnISerAspTYrMetLeuTYrValILyAspTrnThrAlaTnTrnGIn	338
OY	901	CCTCCACAAAC	957
Db	339	ProAlaValnILnISGLyLeuThrGInLeuProAsnSerILaGInGInLeuAspSerGInAsp	358
OY	958	ATCAACAGATTCCGAGCAGGTGAAGAAGGCTCGATTCAGGGCAGCTGATCAT	1008
Db	359	LeuSerAspSerATgAlaGILyGInGInGILySerILeATgAlaValAspILnS	375
RESULT 12			
AAVS3028			
ID	AAVS3028	standard; Protein: 414 AA.	
XX	AAVS3028:		
XX			
XX	29-FEB-2000	(first entry)	
XX			
EX		Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.	

KW	Human; secreted protein; nutritional; cytokine; cell proliferation;
KM	differentiation; immune stimulating; vaccine; suppression;
KV	haematopoiesis regulation; tissue growth; activin; inhibin;
KW	chemotactic; chemokine; haemostatic; thrombolytic; receptor;
KM	ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
KX	tumour inhibition; gene therapy.
OS	Homo sapiens.
XX	
PN	WO957132-A1.
XX	
PD	11-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-US09970.
XX	
PR	07-MAY-1998; 98US-008456A.
PR	02-JUN-1998; 98US-008764S.
PR	22-JUL-1998; 98US-009371Z.
PR	31-JUL-1998; 98US-009493S.
PR	10-AUG-1998; 98US-0095880.
PR	11-AUG-1998; 98US-009606B.
PR	06-MAY-1999; 99US-009606B.
XX	
PA	(GENY) GENETICS INST INC.
PI	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI	Meberry D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;
PI	Diblasio-Smith E, Widom A,
DR	WPI: 2000-052937/04.
DD	N-PDSB: AA233346.
XX	
PT	New polynucleotides encoding secreted human proteins, derived from
PT	adult placenta, adult retina, fetal brain, fetal
XX	
PS	Claim 71: Page 416-417; 492pp: English.
CC	The present invention describes new human secreted proteins which were
CC	isolated from adult placenta, adult retina, foetal brain, foetal kidney
CC	adult blood, adult brain, adult thyroid, adult bladder, adult neural
CC	tissue, adult testes, and adult lymph node cDNA libraries. The human
CC	secreted proteins, and the polynucleotides encoding them, are predicted
CC	to have biological activities which would make them suitable for
CC	treatment, preventing or ameliorating medical conditions in humans and
CC	animals. Suggested activities include nutritional activity, cytokine
CC	and cell proliferation/differentiation activity, immune stimulating
CC	(e.g. as vaccines) or suppressing activity, haematopoiesis regulating
CC	activity, tissue growth activity, activin/inhibin activity,
CC	chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC	activity, receptor/ligand activity, anti-inflammatory activity,
CC	cadherin/tumour invasion suppressor activity, and tumour inhibition
CC	activity. The polynucleotides are also stated to be useful for gene
CC	therapy. AA233316 to AA233373 encode human secreted proteins, and
CC	AA252998 to AA253060 represent human secreted proteins, given in the
CC	present invention.
XX	
SQ	Sequence 414 AA;
XX	
Alignment Scores:	
Pred. No.:	1,88E+135 Length: 414
Score:	1591.00 Matches: 308
Percent Similarity:	91.67% Conservative: 0
Best Local Similarity:	91.67% Mismatches: 0
Query Match:	88.34% Indels: 28
DB:	Gaps: 1
XX	
US-09-778-187B-1_COPY_130_1137 (1-1008) x AAY53028 (1-414)	
QY	1 ATCCCCACAGGTGATGGGCAGAACTCTTTTCGAAAACGCGACAGTATCGAGGAGAG 60
DB	39 IIEPOTIRNGLYASPGLYGLNASHLEUPHEHTRHYSPAVIATHRVALLIEGLINGLYLN 58

OY	61	GTGGGACCATTCAGTTGGCAGCTCAATAATGAAGTGACAGACTCTGTGATTCCAGCTACTGCAT	120
Dd	59	VAlAIAIrrrILleSerCySgInValAsnLysSerAspSpSeValIIlegInLeuEasN	78
OY	121	CCCAACAGGACAGACCATTATTTTAAAGGACTTCAGGCCCTTTGAAGGACACAGATTTCAG	180
Dd	79	rProSAArvgGIrrrILleTyrrPheArgrAspPheArgrProLeuLysAspSerArghPheGln	98
OY	181	TTCGTGAATTTTTTCTAGCAGTGAACCTCAAATATCATTTGACAACCGTTCGAATTTCTGAT	240
Dd	99	LeuLeuAnPhSeSerSerSerGcltLeuLysValSerLeuThraValSerILleSerAsp	118
OY	241	GAAAGAATATCTTTTGGCACCTCTATACCGATCCGCCACAGAAATTTACACCACATC	300
Dd	119	GIugLyArqTYrrPheCySgInLeuTyrrThrasProGlnGlnSerTYrrTrHlle	138
OY	301	ACAGCTCTGGTCCCASCACSTATCTGTGATCATTCGTAAGAAAGACATCGGGGGGAA	360
Dd	139	ThrVAlleuValProPorArghAsnLeuMetILleSplleGlnLysArrrHlAlaValGlu	158
OY	361	GGTGAGAGATTGAAGTCAACTGCATGTCTATGGCCAGCAAGCCAGCCAGCACTATCAG	420
Dd	159	GIugLIugLIuIIeGIuValAsnCysTrHAlaMeTalaserLysProAlaTrHrrrILleArg	178
OY	421	TGGTTCAAGGAGAACACACAGACTAAAAGCCAATCCGAGGTGGAAAGTGTGTACAGATG	480
Dd	179	TrPrHeuLysGIyAsnTrHGIleuLyselLyLSerSerGIuValGIugLuTrTPserAspMet	198
OY	481	TACACTGTGACCAGTACACTGATCTCTGAAGGTGCACAAAGGAGGACGATGGGGTCCAGTG	540
Dd	199	TYrrTrHrrValILlrHrSerGlnMeLeuLysValHisLysGlnLysAspArgLyAlProVal	218
OY	541	ATTCGCCAGGTGGAGCACCCCTGGCGGTCACTGGAAACCTGCAGAACCCAGCGGTACTAGAA	600
Dd	219	IleCySgInValGIuLnIsProAlaValTrHcLySnLeuGlnTrHrgInArGYrrLeuGln	238
OY	601	GTAACGTTAAAGCCTCAAGTGCACATTCACATGACTTATCTCTACAGGCTTAACCCGG	660
Dd	239	ValGIrrTYrrLysProGlnValHisILlegImethTrTYrrProLeuGlnGlyLeuTrHrrArg	258
OY	661	GAAGGGAGCGCGCTTGAACTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTA	720
Dd	259	GIugLyAspAlaLeuGlnLeuTrHCySgInAlaILleGLyLysProGlnProValMetVal	278
OY	721	ACTTGGGTGAGAGTGCATGATGAATGCGCTCAACACGCGCTACTGTTGTGGGCCCAACTG	780
Dd	279	ThrrTrPrrValArqValAspAspGIumeProGlnHISAlaValLeuSerGIyrrProAsnLeu	298
OY	781	TTTCATCATTAACCTTAACAAAAACAGATAATGTTCATACCGCTGTGAAGCTTAAACATA	840
Dd	299	PheILleAsnAsnLeuAsnLysTrHAspAsnGlyTrHtyrArGcySgInAlaSerAsnILle	318
OY	841	GTGGGAAAGCTCACTCGGATTATATCTGTAAATGTATACATGATCCGCCCAACTATCCCT	900
Dd	319	ValGIyLysAlaHisSerAspTYrrMeLeuTyrrValTYrr-----	331
OY	901	CCTCCACACMACACACACACACCCACCCACACACACACACACACACACATCTTACCATCATC	960
Dd	331	-----	331
OY	961	ACAGATTCCGACGACGAGTGAAGAAGCTGCATCAGGGCACTGCATCAT	1008
Dd	332	--AspSerArqAlagIyGIugLIugLyserrILleArqAlaValAspHis	346

RESULT 13
 AAB25593
 ID AAB25593 standard; Protein: 229 AA.
 XX AAB25593:
 XX
 DT 21-NOV-2000 (first entry)
 DE Protein encoded by human secreted protein gene #11 clone H0UDJ81.

XX	Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic; dermatological; antiproliferative; antiarteriosclerotic; antineoplastic; vulnary; antiviral; antibacterial; antifungal; immunoregulatory; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer melanoma; lymphoma; wound healing; human.
XX	Homo sapiens.
XX	WO200029435-A1.
PN	25-MAY-2000.
PD	27-OCT-1999; 99WO-US25031.
XX	28-OCT-1998; 98US-0105971.
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y; Greene JM;
PI	WPI: 2000-387742/33.
XX	Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases -
PT	Claim 1; Page 685-686; 8033p; English.
PS	The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAB066-80623 encode the 12 secreted protein sequences given in AAB25576-825593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic; dermatological; antiproliferative; antiarteriosclerotic; antineoplastic; vulnary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antagonists may be used to treat prevent and/or diagnose various diseases, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraneoplasms and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #1 and protein sequences are represented in sequences AAB0616 and AAB25586. Sequences AAB0677-A80682 represent genes related to the secreted protein gene#11.
CC	Sequence 229 AA;
XX	Alignment Scores:
XX	Pred. NO. 3.44e-97 Length: 229
XX	Score: 1167.50 Matches: 225
XX	Percent Similarity: 98.68% Conservative: 1
XX	Best local Similarity: 98.68% Mismatches: 0
XX	Query Match: 64.83% Indels: 2
DB	11 Gaps: 1
US-09-778-187B-1_COPY_130_1137 (1-1008) x AAB25593 (1-229)	
0Y	ATGATGATATTCAGAAAGACACGCGGTGGAGAGTGAAGTCAACTGCAC 387
Db	1 MettelsprieIgtInlySAsPfhAlaIvalaIgtIuclIgtIuclIgtIuvalaIascySthr 20
0Y	388 GCTATGGCCACCAAGCCAGCCACACACATCATGAGGTTCAAAGGGAACACAGAGCTAAAA 447

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|||||
Db 21 AlamelalaserlyserProalrthrtrileArgtrpPhelysclYasnhrGluleuLys 40
OY 448 GCGAAATCGAGAGTGAGAGAGTGGTGCAGACATGTACACTGTGACGAGTGCAGTGCATGTC 507
Db 41 GlylyserSerGlualcduclutrpSerAspMetTrThValthrSerGlneuMetLeu 60
OY 508 AAGGTGCACAGAGAGAGCATGGGGTCCCAAGTATGTCAGGTGCAGAGCACCTGGCGTC 567
Db 61 LysValthrLysGluAspArgLysValProvalIleCyGsluValclunhrProalVal 80
OY 568 ACTGGAACCTGCAGACCCAGCGGTATGTAGAAGTACAGTATAGCCTCAAGTGCACAT 627
Db 81 ThrGlyAsnLeuGlnThrGlnArgTrpLeuGluValGlnTrpLysProGlnValhrLsle 100
OY 628 CAGATGACTTATTCCTTACAGGCTTACAGCCGGAGAGGAGCGCGCTTGAGTAAACATGT 687
Db 101 GlnMetTrThTrpProLeuGlnGlyLeuThrArgGluAspAlaLeuGluLeuThrCys 120
OY 688 GAAGCCATCGGAGAGCCCGAGCCTGTGATGTAACTTGGGTGAGAGTGCATGTAATG 747
Db 121 GluAlaIleGlyLyspProGlnProValMetValThrTrpValArgValAspArgLumet 140
OY 748 CCTCAACAGCCGCTACTGTCTGGGCCAACCTGTTCATATACCTAAACAACAGAT 807
Db 141 ProGlnHlsAlaValLeuSerGlyProAsnLeuPheIleAsnLeuLysnLysThrAsp 160
OY 808 AATGTGACATACCGCTGTAGAGCTTCAACATAGTGGGAAAGCTACACGCTTATATG 867
Db 161 AanglyThrTrArgGlySerGluAlaSerAsnIleValGlyLysAlaThrSerAspTrMet 180
OY 868 CTGTATGTATACGATCCCGCCACAACTATCCCTCTCCACAAACACACACACAC 927
Db 181 LeuTrValIlyAspProProThrTrhrIleProProProThrTrhrTrhrTrhrTrhr 200
OY 928 ACCACCAACCAACCAACCACTCTTACATCATCATCAGATGCCAGAG---CAGGTGAAGA 984
Db 201 ThrTrhrTrhrTrhrTrhrTrhrIleLeuThrIleIleThrAspSer-ProsSerGlnValLys 220
OY 985 GCGTCGATCAGGAGCATGGATC 1006
Db 220 bAlaArgSerGlyGlnTrpIle 227

RESULT 14
AAM78418
ID AAM78418 standard; Protein; 387 AA.
XX
AC AAM78418;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1080.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
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PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR MPI: 2001-476283/51.
XX
DR N-PSDB: AAK51551.
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3307-3308; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 387 AA:
XX
Alignment Scores:
Pred. No.: 2 21e-48 Length: 387
Score: 629.00 Matches: 124
Percent Similarity: 61.39% Conservative: 62
Best Local Similarity: 40.92% Mismatches: 111
Query Match: 34.93% Indels: 6
DB: 22 Gaps: 3
US-09-778-187b-1_COPY_130_1137 (1-1008) x AAM78418 (1-387)
OY 10 GGTGATGGCGAGAAATCTGTATTACGAAAGACGTGCAGTGCAGAGAGGTTCGGACC 69
Db 21 GYAlaGlyGlnGluValGlnThrGluAsnValThrValAlaGluGlyValAlaGlu 40
OY 70 ATCAGTTGCCAAGTCAATTAAGAGTGCAGACTGTGTATCAGCTACTGAATCCCAAGG 129
Db 41 IleThrCysArgLeuHnIscGlnTrpAspGlySerIleValValIleGlnAsnProAlaArg 60
OY 130 CAGACATTATTATTACAGGGGCTTCAGGCGCTTCGAAAGACAGCGATTTCAGTGAAT 189
Db 61 GlnThrLeuPheHnAsnGlnIlyThrArgAlaLeuLysAspGluArgPheGlnLeuGlu 80
OY 190 TTTTCTAGCAGTGAACSTCAAGAGTATCATTCGACAAACGCTGCAATTTCTGATGAAGAGA 249
Db 81 PheSerProArgArgValArgIleArgLeuSerAspAlaArgLeuGlnAspGluGly 100
OY 250 TACTTTGCCAGCTGTATACCGATCCGCCACAGAAAGTTACACACACATCAGATCTCG 309
Db 101 TyrPheCysGlnLeuIlyThrGluAspTrhHnIscGlnIleAlaThrLeuThrValLeu 120
OY 310 GTCCSACAGSTAACTGATGATCGATATCCAGAAAGACACGCTGGGAGGTGAGAG 369
Db 121 ValAlaProGluAsnProValValGluVal---ArgGluGlnAlaValGluGlyGlu 139
OY 370 ATTGAATCAACTGCAGCTGCTATGGCCAGCAACGCCACGACATGTCAAGTGGTTCAAA 429
Db 140 ValGluLeuSerCysLeuValProArgSerArgProAlaAlaThrLeuArgTrpTrpArg 159
OY 430 GGGACACAGAGCTAAAGGCAAAATCGAGAGGTGGAAGATGGTCAGACATGTACACTGTC 489
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[illegible]

XX		A method for detecting human beta-secretase cleavage of polypeptides
PT		useful for identifying beta-secretase inhibitors
XX		
PS		Examples; Fig 1; 43pp; English.
XX		
CC		This sequence is the human beta-secretase enzyme polynucleotide.
CC		Beta-secretase is capable of cleaving the beta-amyloid precursor prob
CC		(APP) (AAV3742;swedish mutant APP). This enzyme is used in a method
CC		detecting human beta-secretase cleavage of polypeptides and for
CC		identifying beta-secretase inhibitors. The protein has a deduced
CC		molecular weight of 49 kD, although this is without glycosylation and
CC		the expected molecular weight is therefore higher. Inhibition of
CC		beta-secretase activity would be useful for chemical modelling of a
CC		critical event in the pathology of Alzheimer's disease. Inhibitors of
CC		a beta-secretase would be useful for the prevention and treatment of
CC		Alzheimer's disease and Down's Syndrome.
XX		
SQ	Sequence	444 AA;
	Alignment Scores:	
Pred. No.:	7, 23e-48	length: 444
Score:	623.50	Matches: 137
Percent Similarity:	57.83%	Conservative: 66
Best Local Similarity:	39.03%	Mismatches: 121
Query Match:	34.62%	Indels: 27
DB:	20	Gaps: 6
US-09-778-187B-1_COPY_130_1137 (1-1008) x AAV33741 (1-444)		
OY	16 GGGCAGANTCTGTTTACGAAAGCGTGACAGGTGCAGGAGAGGTTCGCCATCACT	75
Db	33 GlyInPheProLeuThrGlnAsnValLthrValAlGluGlyThralAlaIleLeuThr	52
OY	76 TGCCAAGTCATTAAAGAGTGACAGACTCTGTGATTCACGTACTGAATCCCAACAGCAGAC	135
Db	53 CysArfValaIsprGlnAsnAspAsnthSerLeuIdnInrPserAsnProLaIngInltnr	72
OY	136 ATTATATTCCAGGACCTTCAGCCCTTTCAGAGACGCGTTCAGTTGATGCTCATTTTTCT	195
Db	73 LeuTrPheAspAspLySLySaLaLeuArqAspSmrArgIleGluEuVaIArqaLaSer	92
OY	196 AGCAGTAGCTCAAAGTATCATTTGACAACAGCTCTCAATTTCTGATGAAGAAGATCACTT	255
Db	93 TrpHisGluLeuSerIleSerValiserAspValserLeuSerAspGluGlnTythr	112
OY	256 TGCACAGCTCTATACCAGTCCCCACAGAAAGTTACACACCATCACAGTCTCGTCCCA	315
Db	113 CysSerLeuPheThrMetProValLtyrSrhSerLySaLaIatyrLeuThrValLeuGlyVal	132
OY	316 CCACGTAATCTGATGATGATGCATATATCCAGAAAGACATCGGGTGAGAGTGAGATTGAA	375
Db	133 ProGluLysProGlnIleSerGlyPheserSerProValImetGluLysAspleuMetGln	152
OY	376 GTCAACTGCACTGCTATGGCCAGCAGAACCCACGCCAGCATGACAGTGTTCAAAAGGAA	435
Db	153 LeuThrCysLysTrnSerGlySerLyProAlaIalAspIleaArgTrpPheLysAsnaSp	172
OY	436 ACAAGCTAAAAGGCAATCGGAGAGTGGAAGATGGTCA-----GACATGTCACT	486
Db	173 LysGluIleLeuAspValLysTyLeuLysIleuLisAspAlaAsnArgLysTrnPheThr	192
OY	487 GTGACCAAGTAGCGTGAAGTGCAGACGTCACAGAGAGAGCATGGGGTCCAGTGAATCG	546
Db	193 ValSerSerThrLeuAspPheAlaGValaIsprIserAspSpolyAlaIaValIleCys	212
OY	547 CAGGTGAGACCCCTGGCGGTCACTGTGAACCTGCAG---ACCAGCGGATATCAGAAGTA	603
Db	213 ArgValaIsprHisGluSerLeuAsnAlaIthrProGlnValaImetGlnValleuGluIle	232
OY	604 CAGATATAAGCCTCAAGTGCACATTCAGATCACTTATCTCTACAAAGGCTTAACCCGGAA	663
Db	233 HisTrpTrnProSerValLysIle-----IleProSerThrProPheProGlnGlu	249

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OY 664 GGGGACCGCCCTTGAGTTAAATGATGTAAGCCATGCGGAGAGCCCGCTGTGATGTAAC 723
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Job time : 58.25 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:56:11 ; Search time 8.5 seconds

(without alignments)
3714.538 Million cell updates/sec

Title: US-09-778-187b-1_COPY_130_1137

Perfect score: 1801

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 100480 segs, 15661496 residues

Total number of hits satisfying chosen parameters: 200960

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published_Applications_AA:*

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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1761	97.8	440	9	US-09-944-413-61
2	1761	97.8	440	9	US-09-944-403-61
3	1761	97.8	440	9	US-09-944-896-61
4	1761	97.8	440	10	US-09-866-028-61

5	1761	97.8	440	10	US-09-944-449-61	Sequence 61, Appl
6	1761	97.8	440	10	US-09-944-457-61	Sequence 61, Appl
7	1761	97.8	440	10	US-09-944-862-61	Sequence 61, Appl
8	1761	97.8	440	10	US-09-945-587-61	Sequence 61, Appl
9	1761	97.8	440	10	US-09-945-015-61	Sequence 61, Appl
10	1761	97.8	440	10	US-09-944-396-61	Sequence 61, Appl
11	1761	97.8	440	10	US-09-944-097-61	Sequence 61, Appl
12	1761	97.8	440	10	US-09-944-432-61	Sequence 61, Appl
13	1761	97.8	440	10	US-09-943-762-61	Sequence 61, Appl
14	1761	97.8	440	10	US-09-944-654-61	Sequence 61, Appl
15	1761	97.8	440	10	US-09-943-851A-61	Sequence 61, Appl
16	1761	97.8	440	12	US-10-052-586-34	Sequence 34, Appl
17	1761	97.8	442	9	US-09-778-510-20	Sequence 20, Appl
18	1761	97.8	442	9	US-09-778-187B-2	Sequence 2, Appl1
19	1741	96.7	423	9	US-09-778-510-22	Sequence 22, Appl
20	1741	96.7	423	9	US-09-778-187B-4	Sequence 4, Appl1
21	482.5	26.8	398	9	US-10-047-542-79	Sequence 79, Appl
22	482.5	26.8	398	9	US-09-778-510-4	Sequence 4, Appl1
23	471.5	26.2	398	9	US-09-905-291A-84	Sequence 84, Appl
24	471.5	26.2	398	9	US-09-778-510-6	Sequence 6, Appl1
25	471.5	26.2	398	9	US-09-778-187B-10	Sequence 10, Appl
26	471.5	26.2	398	10	US-09-745-763-102	Sequence 102, App
27	471.5	26.2	398	10	US-09-909-320-84	Sequence 84, Appl
28	471.5	26.2	398	10	US-09-909-086B-84	Sequence 84, Appl
29	469.5	26.1	432	9	US-09-778-510-2	Sequence 2, Appl1
30	219	12.2	344	9	US-09-978-187B-8	Sequence 8, Appl1
31	219	12.2	344	9	US-09-978-295A-523	Sequence 523, App
32	219	12.2	344	9	US-09-966-546-4	Sequence 4, Appl1
33	219	12.2	344	9	US-09-966-546-6	Sequence 6, Appl1
34	219	12.2	344	9	US-09-978-697-523	Sequence 523, App
35	219	12.2	518	10	US-09-919-172-20	Sequence 20, Appl
36	218.5	12.1	749	10	US-09-764-853-794	Sequence 794, App
37	218.5	12.1	749	10	US-09-764-853-605	Sequence 605, App
38	214.5	11.9	1115	12	US-10-052-586-440	Sequence 440, App
39	210	11.7	1256	9	US-10-047-542-90	Sequence 90, Appl
40	206	11.4	734	10	US-09-756-551A-17	Sequence 17, Appl
41	205	11.4	737	10	US-09-925-301-1133	Sequence 1133, Ap
42	204	11.3	652	9	US-10-047-542-80	Sequence 80, Appl
43	195.5	10.9	1362	9	US-10-047-542-89	Sequence 89, Appl
44	193.5	10.7	1395	9	US-09-808-602-67	Sequence 67, Appl
45	192.5	10.7	350	9	US-09-808-602-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-944-413-61
Sequence 61, Application US/09944413
Patent No. US2002015604A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvarolf, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25

;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
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;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
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;; ORGANISM: Homo Sapien
US-09-944-413-61

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RESULT 2
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Sequence 61, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
  APPLICANT: Baker, Kevin
  APPLICANT: Botstein, David
  APPLICANT: Eaton, Dan
  APPLICANT: Ferrara, Napoleone
  APPLICANT: Fliviaroff, Ellen
  APPLICANT: Gerritsen, Mary
  APPLICANT: Goddard, Audrey
  APPLICANT: Godowski, Paul
  APPLICANT: Grimaldi, Christopher
  APPLICANT: Gurney, Austin
  APPLICANT: Hillan, Kenneth
  APPLICANT: Kijavlin, Ivar
  APPLICANT: Nepler, Mary
  APPLICANT: Roy, Margaret
  APPLICANT: Tumas, Daniel
  APPLICANT: Wood, William
TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
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PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998

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PRIORITY APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/19330
PRIOR FILING DATE: September 16, 1998
PRIORITY APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIORITY APPLICATION NUMBER: 09/216,021
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PRIORITY APPLICATION NUMBER: 09/218,517
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PRIORITY APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIORITY APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIORITY APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIORITY APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-403-61

Alignment Scores:
Pred. NO.: 7,12e-116 Length: 440
Score: 1761.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
Gaps: 0

US-09-778-1878-1_COPY_130_1137 (1-1008) x US-09-944-403-61 (1-440)
QY 1 ATCCCCACAGGTATGGGCAGAAATCTGTTTACGAAGAAGCGTAGCAGTGAGGAGAG 60
Db | |||||
37 ILEPOTRHCILYASPGILGINASLNPHERHLYSASPVALTHIRVALLIEGLUGLGI 56
| |||||
QY 61 GTTCGAGCCATCACTTCGCCAACATCAATAAAGCTGACAGACTCTGGATTGCGTAAGTAA 120
Db | |||||
57 VALIATRRIIESERYSGINVAISNLSYSERSPASSPERVALLIEGLINLEUASN 76
| |||||
QY 121 CCCAACAAGCAGACATTTATTTTACGGAGCTTACAGCGCTTTGAAGAAGCACAGATTTCAG 180
Db | |||||
77 PROASNNRGTGINTNRILLIETRYPHAIRGPHEARIGPROLEUYSAPSERATGPHEGN 96
| |||||
QY 181 TTGCTGAATTTTTCTAGACAGTGAACCTCAAGATCATTTGACAAACGCTTCAATTTCTGAT 240
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Db	97	LeuLeuAaNPheSerSerSerGclUleuLysValSerLeuThrAsnValSerIleSerAsp	118
QY	241	GAAGGAAACAATCTTTGGCCACCTCTATAACGATCCCCACAGGAAATGTACACACCATC	300
Db	117	GlugLysArgYrPheCysGclLeuYrThrAspProGlnGlnSerYrThrThrIle	136
QY	301	ACAGCTCGTGGCCACACGCACTAATCTGATTCATATCCAGAAAGACACTGGCGGTGAA	360
Db	137	ThrValLeuValProProArgAsnLeuMetIleAspIleGlnYsAspThrAlaValGlu	156
QY	361	GGTAGGAGATTGAAGTCAATGTGCACGTCTATGGCCAGCAAGCCAGCCAGCATATAGG	420
Db	157	GlyGlnGluIleGluValAsnCysThrAlaMetAlaSerYsProAlaThrThrIleArg	176
QY	421	TGGTTCAAGGGAACACACAGACCTTAAAGGCAAAATCCGAGGCGGAAGAGTGTGACATG	480
Db	177	TrpPheYsGclAsnThrGluLeuLysGlyYsSerGclValGluGluTrpSerAspMet	196
QY	481	TACACTGTGACCACTACAGCTGATCTCTAAGGTGCACAGAAGACAGATGGGGTCCAGTG	540
Db	197	TyrThrValThrSerGlnLeuMetLeuLysValHisIlysgLysAspArgValAlProVal	216
QY	541	ATTCGCCAGGCGGAGCAACCCCGGGCTACTGGGAACCTCGAGACCCCGCGGTATCTAGAA	600
Db	217	IleCysGlnValGluHisProAlaValThrGlyAsnLeuGlnThrGlnArgYrLeuGlu	236
QY	601	GTACAGTATAAGCCCTCAAGTGCACATTCAGATGACTTATCTCTACAGAGCTTAACCCGG	660
Db	237	ValGlnYrYlYsProGlnValHisIleGlnMetYrYrProLeuGlnGlyLeuThrArg	256
QY	661	GAAGGGAGCGGGCTTGAGTTTACAATGTGGAAGCCATCCGGAAGCCCCAGCCTGTGATGTGA	720
Db	257	GluGlyAspAlaLeuGluLeuThrCysGlnAlaIleGlyLysProGlnProValMetVal	276
QY	721	ACTTGGGTGAGAGTTCGATGTGTAAGTAATCCTCAACACGCCCTACTGTCTGGGCCAACCTG	780
Db	277	ThrTrpValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu	296
QY	781	TTTCATCAATTAACCTTAAACAAACAGATAATGTGTCATACCGCTGTGAAGCTTAAACATA	840
Db	297	PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrYrArgCysGlnAlaSerAsnIle	316
QY	841	GTGGGGAAGCTCACTCGGATATATCTGTATGCTATAGCATCCCCACACATATACCTT	900
Db	317	ValGlyLysAlaHisSerAspYrMetLeuYrValYrAspProProThrThrIlePro	336
QY	901	CTTCCCAACAACACACACCACACACACACACACACACACACACATCTTACCATCATC	960
Db	337	ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleuThrIleIle	356
QY	961	ACAAATTCGCGAGCAGGTGAAGAAAGCTGCATCAGGCACTGGATCAT 1008	
Db	357	ThrAspSerArgLagIlyGluGlnGlySerIleArgAlaValAspHis 372	
RESULT 3			
US-09-944-896-61			
: Sequence 61, Application us/09944896			
: Patient No. US20020168715A1			
: GENERAL INFORMATION:			
: APPLICANT: Baker, Kevin			
: APPLICANT: Bolstein, David			
: APPLICANT: Eaton, Dan			
: APPLICANT: Ferrara, Napoleone			
: APPLICANT: Filvaroff, Ellen			
: APPLICANT: Geriltsen, Mary			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Godowski, Paul			
: APPLICANT: Grimaldi, Christopher			
: APPLICANT: Gurney, Austin			
: APPLICANT: Hillan, Kenneth			
: APPLICANT: Kijavon, Iyar			
: APPLICANT: Napier, Mary			
: APPLICANT: Roy, Margaret			

;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: May 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-896-61

Alignment Scores:

Pred. No.:	7,12e-116	Length:	440
Score:	1761.00	Matches:	336
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.78%	Indels:	0
DB:	9	Gaps:	0

US-09-778-187b-1_copy_130_1137 (1-1008) x US-09-944-896-61 (1-440)

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Db 37 TLeProthrgLyAspPolYgInAsnLeuPheThrLyAspValThrvAlLlegLugLyGu 56
Oy 61 GTTGGCAGCATGATGTTGCCAAGTCAATTAAGAGTACAGCTGTGTGATTGACTAGTGAAT 120
Db 57 VALAlAThrlLeserCysGlnValAsnLysSerAspSperValLlegLInLeuAsn 76
Oy 121 CCCACAGCAGACCATTAATTTCAGGGACTTCAGCCCTTTGAGAGACGAGCTTTCAG 180
Db 77 ProAsnArGdlThrlrLerYrPheArGAspPheArGPrLeuLysAspSerArGpHeGln 96
Oy 181 TTGCTGAATTTTTTTCAGAGTGAAGTCAAGTATTCATTAACAGCTCTCAATTTCTGAT 240
Db 97 LeuLeuAsnPheserSerSerGlnLeuLysValSerLeuThrvAsnValSerLieserAsp 116
Oy 241 GAGAGAGTACTTTTGGCAGCTCTATACCGATCCCGCCAGAGAAAGTACACACCATC 300
Db 117 GlnGlnYArGtYrPheCysGlnLeuYrThrvAspProGlnGlnSerYrThrvThrlle 136
Oy 301 ACAGTCCGTGCTCCACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 137 ThrvAlLeuValProProArGAsnLeuMetLiesPileGlnLysAspThrvAlaValGln 156
Oy 361 GGTGAGGAGATTGAAGTCAACTGCACTGCTATGGCCAGCAGCAGCAGCATATCAGG 420
Db 157 GlnGlnGlnLlLlegLInValAsnCyStrAlaMetLaserLysProAlarThrvThrlleArG 176
Oy 421 TGGTTCAAGGAGACAGACAGTAAAGCAATGCGAGAGTGAAGAGTGGTCAGCATG 480
Db 177 TrPpHeLysGlnYArThrvLleuLysGlnYrSerGlnValGlnLlLlrvTrPserAspMet 196
Oy 481 TACACTGTGACAGTACAGTGTGAGAGTGCACAAAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 197 YrThrvThrvAlThrvSerClnLeuMetLysValHlsLysGlnAspSplyValProVal 216
Oy 541 ATCTGCCAGGTGAGACAGCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGA 600
Db 217 LlecYsgInValGlnLlLlrvProAlaValThrvGlnYrAsnLeuGlnThrvClnArGtYrLleGln 236
Oy 601 GATACAGTATAACGCTCAATGACATGACATGACATGACATGACATGACATGACATGAC 660
Db 237 VALGlnYrLysProGlnValHlsLlegLlnMetThrvTrProLeuGlnGlnLlLlrvThrvArG 256
Oy 661 GAAGGAGAGCGCTTGAAGTAAATGATGAAAGCATGCGAGAGAGAGAGAGAGAGAGAGAG 720
Db 257 GlnGlnYrAspAlaLeuGlnLeuThrvCysGlnAlaLlLlegLlLysProGlnProValHlMetVal 276

Oy 721 ACTTGGGTAGAGTGCATGATGAATGCTTCAACAGCCCGTACTGTGTGGCCCAACTTG 780
Db 277 ThrvTrPvalArGValAspAspGlnMetProGlnHlsAlaValLeuSerGlnProAsnLeu 296
Oy 781 TTCATCAATTAACCTTAACAAACAGATATGGTACCTACCGCGTGAAGTCTTAACACATA 840
Db 297 PheLlAsnAsnLeuAsnLysStrAspAsnGlnYrThrvArGysGlnLlLlrvAsnLlLle 316
Oy 841 GTGGGGAAGCTCACTCGGATATATGCTGTATGTATAGATCCCGCCCAACTATCCCT 900
Db 317 VALGlnYrLysAlaHlsSerAspTrpYrMetLeuYrValYrAspProArGThrvThrllePro 336
Oy 901 CCTCCACACAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTATC 960
Db 337 ProProThrvThrvThrvThrvThrvThrvThrvThrvThrvThrvThrvThrvThrvThrv 356
Oy 961 ACAGATTCGCCGACGAGCTGAAGAAGCTGATGATGATGATGATGATGATGATGATGAT 1008
Db 357 ThrvAspSerArGAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 372

RESULT 4
US-09-866-028-61

;; Sequence 61, Application US/09866028
;; Patent No. US20020058309A1
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Baton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerltsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kijavln, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548PICI
;; CURRENT APPLICATION NUMBER: US/09/866,028

;; PRIORITY FILING DATE: 2001-05-25
;; PRIOR APPLICATION data removed - consult PALM or file wrapper

;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61

;; LENGTH: 440
;; TYPE: PRT

;; ORGANISM: Homo Sapien
US-09-866-028-61

Alignment Scores:

Pred. No.:	7,12e-116	Length:	440
Score:	1761.00	Matches:	336
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.78%	Indels:	0
DB:	10	Gaps:	0

US-09-778-187b-1_copy_130_1137 (1-1008) x US-09-866-028-61 (1-440)

Oy 1 ATCCCCACAGGTGATGGCGAGATCTGTTTACGAAAGAGCTGACAGTGCAGGAGAG 60
Db 37 TLeProthrgLyAspPolYgInAsnLeuPheThrLyAspValThrvAlLlegLugLyGu 56
Oy 61 GTTGGCAGCATGATGTTGCCAAGTCAATTAAGAGTACAGCTGTGTGATTGACTAGTGAAT 120
Db 57 VALAlAThrlLeserCysGlnValAsnLysSerAspSperValLlegLInLeuAsn 76
Oy 121 CCCACAGCAGACCATTAATTTCAGGGACTTCAGCCCTTTGAGAGACGAGCTTTCAG 180

Db 77 ProasnarGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 96
QY 181 TTGCTGAATTTTCTACAGAGAACCTAAAGTATCATTCAGCAAAAGCTCAATTCATGAT 240
Db 97 LeuLeuAsnSphSerSerSerGluLeuLysValSerLeuThrAsnValSerIleSerAsp 116
QY 241 GAAGGAAGATACCTTTGCGAGCTCTATACGATCCCCACAGAAAGTATACACCACCATC 300
Db 117 GUGUGTyrGlyrPheCysGlnLeuTyrThrAspProProGlnGlnSerTyrThrThrIle 136
QY 301 ACAGTCTGCTCCACACAGTAATCTGATGATATCCAGAAAGCACTGCGGTGGAA 360
Db 137 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 156
QY 361 GGTGAGAGATTTGAAGTCACTGCTATGAGCCAGCAAGCCAGCCAGCATATACAGG 420
Db 157 GUGUGlnGluIleGluValAlaCysThrAlaMetAlaSerLysProAlaThrThrIleArg 176
QY 421 TGGTTCAAAGGGAACACAGAGCTAAAGGCAAAATCGAGGTGAAGAGTGGTCAGACATG 480
Db 177 TrpPheLysGlnAsnThrGlnLeuLysGlyLysSerGluValGlnGlnLutProSerAspMet 196
QY 481 TACAGCTGACCAATGCGTGCATGCTGAAGTGCACAAAGAGACATGGGGTCCCATG 540
Db 197 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGluAspAspGlyValProVal 216
QY 541 ATCTGCAGGTGGAGACACCTGCGGTCTACGTGAGAAACCTGAGACCCGCGGTATCTAGAA 600
Db 217 IleCysGlnValGlnHisProAlaValThrGlyAsnLeuGlnThrGlnAlaGlyTyrLeuGlu 236
QY 601 GTACAGATATAAGCTCAAGTGCACATTCAGATGACTTATCCTTCAAGGCTTAACCCGG 660
Db 237 ValGlnTyrLysProGlnValHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 256
QY 661 GAAGGGAGCGGCTGAGTAAACATGAGCAACCATCGGGAAAGCCCGCTGTGATGCTA 720
Db 257 GUGUGLysAspAlaLeuGlnLeuThrCysGluAlaIleGlyLysProGlnProValMetVal 276
QY 721 ACTTGGGTGAGAGTGCATGATGAATGCTCAACACCGCTACTGTGTGGCCCAACCTG 780
Db 277 ThrTyrAlaArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
QY 781 TTGATCATATACCTAAACAAACAGATATAGTACATACCGCTGTGAAGCTTCAACATA 840
Db 297 PheIleAsnSphLeuAsnLysThrAspAsnGlyThrTyrArgCysGluAlaSerAsnIle 316
QY 841 GTGGGGAACCTGACCTCGATATATGCTGTATGATATACATCCCCCACAACATATCCT 900
Db 317 ValGlyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProProThrThrIlePro 336
QY 901 CCTCCACAACAACACACACACACACACACACACACACACACATCTTACATCATC 960
Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 356
QY 961 ACAGATCCCGAGCAGGTGAAGAGCTCGATCAGGCGCATGATCAT 1008
Db 357 ThrAspSerArgAlaGlyGlnGlySerIleArgAlaValAspHis 372

RESULT 5
US-09-944-449-61
Sequence 61, Application US/09944449
Patent No. US20020102647A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tomas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565

;; PRIOR APPLICATION NUMBER: 60/069, 873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068, 017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070, 440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074, 086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074, 092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075, 945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112, 850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113, 296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146, 222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216, 021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218, 517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254, 311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020110859A1member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020110859A1member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-457-61

Alignment Scores:
Pred. No.: 7, 12e-116 Length: 440
Score: 1761.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 10 Gaps: 0

US-09-778-187b-1_copy_130_1137 (1-1008) x US-09-944-457-61 (1-440)

QY 1 ATCCCAAGGTGATGGGAGAAATCTGTTACGAAGAAGCTGACATGATCGAGGAG 60
Db 37 ILeRrthrgLyspGlyGlnAsnLeuPheThrLysaspAlaThrValILeGLuGLu 56
QY 61 GTTCCGACCATCAGTTGCCAAGTCAATAAGAGTACACACTCTGTGATTCAGTCTAAT 120
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QY 121 CCCAAGGAGGACACCATTTTATTCAGGACCTTCAGGCTTTGAAGGACACAGATTTCAG 180
Db 77 ProAsnArgGlnThrILeThrPheArgAspPheArgProLeuLysAspSerArgPheGln 96
QY 181 TTGCTGAATTTTCTACAGTGAACCTCAAGTATCATTTGCAACGTTCAATTTTGAT 240
Db 97 LeuLeuAsnPheSerSerSerGlnLeuLysValSerLeuThrAsnValSerILeSerAsp 116
QY 241 GAAGGAAGATCTTTTCCAGCTCTATACGATCCCCCAGAGAAATTCACACCATC 300
Db 117 GlnGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 136
QY 301 ACAGTCTGGTCCACACGTAATCTGATGATGATTCAGAAAGACACTGGGCTGGA 360
Db 137 ThrValLeuValProProAlaGlnLeuMetCileAspILeGlnLysAspThrAlaValGlu 156
QY 361 GGTGAGAGATTGAAGTCAACTGCACCTGATGCGCCAGCAAGCCACGACACTATCAG 420
Db 157 GlyGlnLeuILeGlnValAsnLysThrAlaMetAlaSerLysProAlaThrThrILeArg 176
QY 421 TCGTCAAGGAGAACACAGACGCTAAAGGCAATCGAGGTGAAGGTGTACAGCATG 480
Db 177 TrpPheLysGlyAsnThrGlnLeuLysGlyLysSerILeValGlnGluTrpSerAspMet 196
QY 481 TACCTGTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 197 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnLysAspGlyValProVal 216
QY 541 ATCTGCAGGTGAGACACCTCGCGGTCACTGGAACCTGCAGACCCAGCGTATCTAGAA 600
Db 217 ILeGlnValGlnHisPProAlaValThrGlyAsnLeuGlnThrGlnArgTyrLeuGlu 236
QY 601 GTACAGTATAGCTCAAGTGCACATTCAGATGACTTATCTCTACAGGCTTAACCCG 660
Db 237 ValGlnTyrLysProGlnValHisILeGlnMetThrTyrProLeuGlnGlnTyrArg 256
QY 661 GAAGGGAGCGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 257 GlnGlyAspAlaLeuGlnLeuThrCysGlnAlaILeGlyLysProGlnProValMetVal 276
QY 721 ACTTGGGTGAGTGCATGATGAATGCTCAACACGCCGTACTGTCTGGGCCAACCTG 780
Db 277 ThrTrpValArgValAspAspGlnMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
QY 781 TTGATCATATACCTAAACAACAACAGATATGATGATACATCCGCTGTGAAGCTTAACATA 840
Db 297 PheILeAsnAsnLeuAsnLysTrpAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 316
QY 841 GTGGGAAAGCTCACTCGATGATATATCTGATGATATACATGATCCCCCACAATATCCCT 900
Db 317 ValGlyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProProThrThrILePro 336
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Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrILe 356
QY 961 ACAGATTCGCGACAGGTGAAGAAGCTGCATGACGGCAATGATCAT 1008
Db 357 ThrAspSerArgAlaGlyGlnGlnGlySerILeArgAlaValAspHis 372
RESULT 7
US-09-944-862-61
; Sequence 61, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Batstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Klyavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2348P1C1
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
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PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR APPLICATION NUMBER: 60/069,425
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PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
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PRIOR APPLICATION NUMBER: 60/112,850
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PRIOR APPLICATION NUMBER: 60/113,296
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PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Saplen
US-09-944-862-61
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Pred. No.: 7,12e-116 Length: 440
Score: 1761.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
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? PRIOR APPLICATION NUMBER: PCT/US00/20710
? PRIOR FILING DATE: July 28, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/32678
? PRIOR FILING DATE: December 1, 2000
? PRIOR APPLICATION NUMBER: PCT/US01/06520
? NUMBER OF SEQ ID NOS: 120
? SEQ ID NO 61
? LENGTH: 440
? TYPE: PRT
? ORGANISM: Homo Sapien
? US-09-945-015-61

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Alignment Scores:		
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Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	97.78%	Indels: 0
DB:	10	Gaps: 0

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QY	61	GTTTCGACCAATCAGTTCGCAATGCAATAGAGTACACACTCTGATTCAGTCACTGAT	120
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QY	121	CCCAACAGCGACACATTTATTTTCAGGAGCTTCAGGCCCTTTGAAGACAGACAGTTTCAG	180
Db	77	ProAsnArgGlnThrIleIlyPheArgAspPheArgProLeuIysAspSerArgPheGln	96
QY	181	TTTGCTGAATTTTTCAGACGTGAAGCTAAAGTATCATTTGACAAACGTCCTCAATTTCTGAT	240
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QY	241	GAAAGAAATACCTTTTGGCAGCTTATATACCGATCCCCACACAGGAAATTCACACCACATC	300
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[illegible]

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US-09-944-396-61
: Sequence 61, Application US/09944396
: Patent No. US20020132981A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944, 396
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866, 028
: PRIOR FILING DATE: 2001-09-25

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;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
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;; PRIOR FILING DATE: July 28, 1999
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;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO: 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-396-61

Alignment Scores:
Pred. No.: 7,12e-116 Length: 440
Score: 1761.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 10 Gaps: 0

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QY 241 GAAGGAAGATACCTTTGGCCAGCTATACCGATCCCAAGGAAAGTTACACCATC 300
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DB 137 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLYsAspThrAlaValGlu 156
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QY 361 GGTGAGAGATTGAAGTCAACTGACTGATGAGCCAGCAAGCCAGCAGCATTCAGG 420
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DB 157 GlnGluGlnIleGluValAsnCysThrAlaMetAlaSerLYsProAlaThrThrIleArg 176
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QY 421 TGCTTCAAGAGCAACACAGCATGTAAGCAATTCGAGGTGGAAGTGTGACAGATG 480
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QY 481 TTAACGTGACAGTCAAGTCAATGTAAGGTGCACAAAGAGAGAGTGGGTCCAGTG 540
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QY 961 ACAGATCCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1008
Db 357 ThrAsperatGAlaGlyGluGluGlySerIleArgAlaValAspHis 372

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; Patent No. US20020133675A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
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; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F2348P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 097
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
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; PRIOR FILING DATE: May 22, 2000
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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 26, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-097-61

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Pred. No.: 7.12e-116 Length: 440
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 97.78% Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 10 Gaps: 0

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;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
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;; ORGANISM: Homo Sapien
US-09-944-432-61

Alignment Scores:

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US-09-778-187b-1_COPY_130_1137 (1-1008) x US-09-944-432-61 (1-440)

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Db 57 Valalathrllesercysglnvalasnlyssersaspservalilleglinleuasn 76
QY 121 CCCAAGGAGGACCATTTATTTACAGGACTCAGGCTTGAAGGACAGAGGTTTCAG 180
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Db 157 GlygluclullegluvalasnlysthrAlametalaserlysproalathrthllearg 176
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QY 541 ATCTGACAGGTGAGACACCTGGGCTCATCTGAAACCTGACAGACCCAGCGGTATCTGAA 600
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RESULT 13

US-09-943-762-61

;; Sequence 61, Application US/09943762
;; Patent No. US20020142958a1

GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrari, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Geriltsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/943,762
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
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;; PRIOR FILING DATE: December 16, 1997
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;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086


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: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-943-762-61

Alignment Scores:
Pred. No.: 7,12e-116 Length: 440
Score: 1761.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
DB: 10 Gaps: 0

US-09-778-187b-1_copy_130_1137 (1-1008) x US-09-943-762-61 (1-440)

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QY 241 GAAGAAGATATCTTTTGGCAGCTCTATACCGATCCCCACAGAGAAAGTTAACACACCATC 300
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QY 301 ACAGTCTGTCGCCACACACAGTAACTGATGATGATGATGATGATGATGATGATGATGATG 360
DB 137 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 156
QY 361 GGTGAGAGACATTTGAATCAACCTGCTGATGCGCCAGACAGACAGCCAGCATATACAG 420
DB 157 GlyGluGlnIleGlnValAlaAsnLysThrAlaMetAlaSerLysProAlaThrThrIleArg 176
QY 421 TGGTTCAAGAGGACACAGACAGCTAAAGGCAATCGAGGTGGAAGAGTGCACAGATG 480
DB 177 ThrPheLysGlyAsnThrGluLeuLysGlyLysSerGluValGluIleThrPheSerAspMet 196
QY 481 TACACTGTGACACAGTACGATGATGCTGAAGGTGCACACAGAGAGAGATGGGTCCAGATG 540
DB 197 TTTTThrValThrSerGlnLeuMetLeuLysValIleLysGlnLysAspGlyValProVal 216
QY 541 ATTCGCCAGGTGAGACACCTGCGGTCACCTGGAACCTGCAAGCCCAAGCGGTATCTAGAA 600
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QY 601 GTACAGTATTAAGCCTCAAGTCAATTCAGATGACTTATTCAGAGGCTTAAAGGCTTAAAGCCGG 660
DB 237 ValGlnTyrLysProGlnValAlaIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 256
QY 661 GAAGGGAGCGCGCTTGAAGTTAAACATGTGAAGCCATCGGGAAGCCCGACCTGTGATGTA 720
DB 257 GluGlyAspAlaLeuGlnLeuThrCysGlnAlaIleGlyLysProGlnProAlaMetVal 276
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DB 277 ThrThrValAlaArgValAlaAspAspGlnMetProGlnIleAlaValIleuSerGlyProAlaLeu 296
QY 781 TTTCATGAATTAACCTTAACAAACAGATTAATGTACATACCGCTGTGAAGCTTCAACATTA 840
DB 297 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 316
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QY 961 ACAGATTCCCGAGCAGGTGAAGAAGCTCGATCAGGAGGACAGTATCCAT 1008
DB 357 ThrAspSerArgAlaGlyGluGlnGlySerIleIleArgAlaValAlaAspHis 372

RESULT 14
US-09-944-654-61
: Sequence 61, Application US/09944654
: Patent No. US20020142959A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Baton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Flivaeroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
```

APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillab, Kenneth
APPLICANT: Kijavini, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,378
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PRIOR APPLICATION NUMBER: 60/069,425
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PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
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PRIOR APPLICATION NUMBER: 60/113,296
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PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020142959A1member 30, 1999
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PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
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PRIOR FILING DATE: December 16, 1999
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PRIOR FILING DATE: February 11, 2000
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PRIOR FILING DATE: February 22, 2000
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PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-654-61

Alignment Scores:
Pred. No.: 7.12e-116 Length: 440
Score: 1761.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.78% Indels: 0
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Db 237 ValGlnTyrrIlyProGlnValHisIleGlnMetTyrrProLeuGlnIlyLeuThrArg 256
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Db 357 ThrAspSerArgAlaGlyGlnIlySerIleArgAlaValAspHis 372
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Job time: 20 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 ; Search time 12.5 Seconds
(without alignments)
790.888 Million cell updates/sec

Title: US-09-778-187B-2_COPY_39_374

Perfect score: 1761

Sequence: 1 IPTDQGNLFTKDYTVIEG.....LTITDSRAGEGSIKAVDH 336

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	623.5	35.4	421	US-08-660-531-1	Sequence 1, Appl
3	623.5	35.4	444	US-08-659-984A-5	Sequence 5, Appl
4	623.5	35.4	444	US-08-660-531-5	Sequence 5, Appl
5	232	13.2	393	US-08-429-742-2	Sequence 2, Appl
6	212.5	12.1	458	US-09-435-956A-1	Sequence 4, Appl
7	206.5	11.7	388	US-08-429-742-4	Sequence 1, Appl
8	206	11.7	642	US-08-217-299-1	Sequence 36, Appl
9	206	11.7	698	US-08-602-723-36	Sequence 17, Appl
10	206	11.7	734	US-08-389-455A-17	Sequence 18, Appl
11	206	11.7	734	US-08-987-867A-17	Sequence 17, Appl
12	194	11.0	1651	US-09-540-245A-18	Sequence 15, Appl
13	193.5	11.0	1395	US-09-540-245A-15	Sequence 2, Appl
14	192.5	10.9	1241	US-09-040-774-2	Sequence 2, Appl
15	187.5	10.6	583	US-08-432-016-2	Sequence 2, Appl
16	187.5	10.6	583	US-08-684-594-2	Sequence 46, Appl
17	185.5	10.5	308	US-08-414-657D-46	Sequence 2, Appl
18	185.5	10.5	325	US-08-414-657D-2	Sequence 41, Appl
19	185.5	10.5	325	US-08-414-657D-41	Sequence 41, Appl
20	185.5	10.5	325	US-09-135-080-2	Sequence 48, Appl
21	185	10.5	287	US-08-414-657D-48	Sequence 48, Appl
22	183.5	10.4	304	US-08-414-657D-44	Sequence 42, Appl
23	183.5	10.4	315	US-08-414-657D-47	Sequence 43, Appl
24	183.5	10.4	338	US-08-414-657D-42	Sequence 43, Appl
25	183.5	10.4	338	US-08-414-657D-43	Sequence 4, Appl
26	183.5	10.4	338	US-09-135-080-4	Sequence 49, Appl
27	183	10.4	287	US-08-414-657D-49	

28	183	10.4	310	2	US-08-414-657D-45	Sequence 45, Appl
29	182.5	10.4	477	2	US-08-432-016-3	Sequence 3, Appl
30	182.5	10.4	477	2	US-08-684-594-3	Sequence 3, Appl
31	179.5	10.2	1297	4	US-09-540-245A-17	Sequence 17, Appl
32	179	10.2	1447	4	US-09-041-886-25	Sequence 25, Appl
33	179	10.2	1447	5	PCT-US94-05277-2	Sequence 2, Appl
34	178	10.1	869	1	US-08-374-834-16	Sequence 16, Appl
35	178	10.1	869	2	US-08-644-271-29	Sequence 29, Appl
36	178	10.1	869	4	US-09-077-955-33	Sequence 33, Appl
37	177.5	10.1	338	2	US-08-414-657D-60	Sequence 60, Appl
38	177.5	10.1	338	4	US-09-135-080-8	Sequence 8, Appl
39	176.5	10.0	478	5	PCT-US95-08493-15	Sequence 15, Appl
40	176.5	10.0	860	5	PCT-US95-08493-19	Sequence 19, Appl
41	176.5	10.0	868	5	PCT-US95-08493-21	Sequence 21, Appl
42	175.5	10.0	408	4	US-09-724-864-62	Sequence 62, Appl
43	174	9.9	607	2	US-08-752-307B-12	Sequence 12, Appl
44	174	9.9	607	4	US-09-707-802-12	Sequence 12, Appl
45	174	9.9	607	4	US-09-991-326-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-984A-1

Query Match 35.4%; Score 623.5; DB 2; Length 421;
Best Local Similarity 39.0%; Pred. No. 1.1e-46;
Matches 137; Conservative 66; Mismatches 121; Indels 27; Gaps 6;

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QY	6	GONLFTKDVTYIEGEVATYISCOVYNKSDSVIOLLPNROTIFYRDFRPLKDSRFOLLNFS	65							
Db	10	GFPLTONTWYVEGGTALITTCRVDDNDNTSLQMSNPAAQOTIFYFDDKALKALRDRIELTVRAS	69							
QY	66	SEELKAVSLTNVISIDEGRFECOLYLDHPQESTITTYLVLPRLNLMIDIOKOTAVEGEETE	125							
Db	70	WHELSISVSDVSLSEGGQVTCSLFTMPYKTSAAVLYLVGLGVPKPOISGFSFSPVMEGDLQ	129							
QY	126	VNCTAMASKPATTIYMPFKGNTLCKKSEVEEMS---DMYTVSOLMLKHKREDDGVAVIC	182							
Db	130	LTCRKTSKGRPADIDIMFKPKDKETIKDYKVLKEDANKRKTFTYSSITLDFRKRSDDGVAAYIC	189							
QY	183	QVHEPAVYTGNIQ--TQRYLEVOYKPOVNIQMTYPLQGLTREGDALELTGEAIKPOPVAVYT	241							
Db	190	RVDHESLNAITPQVAMQVLEIHYYTSVKI--IPSPRPQEGPLITLTCSSKGRPLREPYLV	246							
QY	242	WVRVUDEM--FOHAYVLSGPNLFINMLKNTDNGTYRCESANIVGAKHSDMYLVYQRPPTI	299							
Db	247	WTKDGELPDPDRMVAVSSGRELNIPLFNAITDNGTYRCETINTTGGQSAEYVLIVHDVPNTL	306							
QY	300	PEPTTTTTTTTTTTTTLTIIR-----DSRAGEEGSIRAVDH	336							
Db	307	LEPTTIIPSLTATVTITTYVAITTSPTTSATTSIRDPNALAGONGP---DH	353							

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RESULT 3
US-08-659-984A-5
: Sequence 5, Application US/08659984A
: Patent No. 5942400
: GENERAL INFORMATION:
: APPLICANT: Anderson, John P.
: APPLICANT: Sinha, Sukanto
: APPLICANT: Jacobson-Croak, Kirsten L.
: TITLE OF INVENTION: Assays for Detecting Beta-Secretase Activity
: TITLE OF INVENTION: Inhibition
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Crew LLP
: STREET: Two Embarcadero Cir., 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/659,984A
: FILING DATE: 07-JUN-1996
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/485,152
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Heslin, James M.
: REGISTRATION NUMBER: 29,541
: REFERENCE/DOCKET NUMBER: 15270-00281005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-659-984A-5

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 ; Search time 15 Seconds

(without alignments)
2153.411 Million cell updates/sec

Title: US-09-778-187b-2_COPY_39_374

Perfect score: 1761

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	263.5	15.0	5175	2 T20992	hypothetical prote
2	263.5	15.0	5198	2 T43290	hemiscitin precurs
3	248	14.1	407	2 T08732	hypothetical prote
4	243	13.8	725	2 JER0099	neural cell adhesi
5	239	13.6	1088	1 IJXLNL	neural cell adhesi
6	227	12.9	4162	2 T42633	connectin/titin -
7	224	12.7	530	2 A53437	poliovirus recepto
8	223.5	12.7	7962	2 J83466	elastic titin - hu
9	223	12.7	725	2 JEO100	neural cell adhesi
10	223	12.7	1092	1 JN0635	neural cell adhesi
11	222	12.6	344	2 I36531	neurotrophin - rat
12	222	12.6	467	1 HLMSP3	poliovirus recepto
13	221	12.5	392	2 B44194	poliovirus recepto
14	221	12.5	417	2 A44194	poliovirus recepto
15	221	12.5	538	2 I68093	PRR2 delta - human
16	219	12.4	518	2 JCA024	poliovirus recepto
17	218	12.4	392	1 KWHUPD	poliovirus recepto
18	218	12.3	417	1 RWHUPA	poliovirus recepto
19	216	12.3	478	2 I53960	PRR2 alpha - human
20	214	12.2	4391	2 A38096	perlecan precursor
21	213.5	12.1	812	2 B42632	cell adhesion mole
22	213.5	12.1	932	2 A42632	cell adhesion mole
23	210.5	11.0	345	2 S03199	oploid-binding pro
24	210	11.0	1011	2 T13669	neuromusculin - fr
25	209.5	11.9	584	2 I50419	s-glycerin precurs
26	208.5	11.8	345	2 JCA025	oploid-binding cel
27	206	11.7	702	2 A36319	carcinoembryonic a
28	203.5	11.6	765	2 C42632	cell adhesion mole
29	202.5	11.5	345	2 JCI239	oploid-binding pro

30	202.5	11.5	862	2 I49583	differentiation an
31	202.5	11.5	868	2 A46512	CD22 homolog/B lym
32	202	11.5	847	2 JH0371	B-cell adhesion pr
33	202	11.5	1443	2 I50600	neogenin - chicken
34	201.5	11.4	338	2 JCI238	oploid-binding pro
35	200	11.4	1323	2 PN0568	connectin 3B - chl
36	197.5	11.2	3707	2 S18252	heparan sulfate pr
37	195.5	11.1	1091	1 IJCHNL	neural cell adhesi
38	195	11.1	1612	2 T30805	ducal protein - mo
39	194	11.0	338	2 JC5519	50K glycoprotein p
40	193	11.0	761	1 IJHUNG	neural cell adhesi
41	193	11.0	1344	2 T14316	rig-1 protein - mo
42	192.5	10.9	1241	2 T37190	neprtin - human
43	191.5	10.9	976	2 T29583	hypothetical prote
44	189.5	10.8	646	2 I38049	cell surface glyco
45	189	10.7	1036	2 S22383	axonin 1 precursor

ALIGNMENTS

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hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20992; T24733
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5175 <MT>
A:Cross-references: EMBL:Z47068; PIDN:CA87335.1; GSPDB:GN00028; CESP:F15G9.4a
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24733
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5175 <MT>
A:Cross-references: EMBL:Z47070; PIDN:CA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone T09B9
A:Gene: CESP:F15G9.4a
A:Map position: X
A:introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 50
Query Match 15.0% Score 263.5; DB 2; Length 5175;
Best Local Similarity 24.6% Pred. No. 6; 2e-10;
Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;
QY 14 VVYIEGEVATISQCVKNSDDSVTQLNPNRQTYFPDFRPL-----KDSRFQLNFSSET 69
DB 2200 VYAIKGAALPKCPID--DDK-----NFGQITILRNYPIDLEADAKITRL---SNDR 2249
QY 70 KVSITNVSISDEGRFCQLYTDPQESYT-TTIVLVPPLNLMIDIOKD-TAVGEIEVN 127
DB 2250 RTILNVTENDEGOYSCRVKNADGENSFDFKATVIVPPTIMLDKDKNKTAVERHSVTLS 2309
QY 128 CRAMSKRPATITRMFG-----NTELKGSKEVERMSDMYVTVSQMLKVKR 173
DB 2310 CPA-TGKRPEDITWFKDGAIHENIADIIPNGELNG-----NOLKTRIRK 2354
QY 174 EDDGVVICOVEHPAVTGMLOTORILEYQKPOVH---TOMTYPLQGLRREGDALETCE 230
DB 2355 EGDAGKYTCEADNSA--GSVEDQVNVNVTITRIKIEDGIPSDYESQ---QNERVYISCP 2408
QY 231 AIGKPPQVWVWTVRVDEMPQHAVL---SGPPLFTNNLNKTDNGTRYCEASNIYKAHS 286

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OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:42 ; Search time 9 Seconds

(without alignments)
1548.450 Million cell updates/sec

Title: US-09-778-187b-2_COPY_39_374

Perfect score: 1761
Sequence: 1 IPTDGGNLTFRDVTYIEG.....LTITDSKAGEGSRVAVDH 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	239	13.6	1088	NCAL_XENLA	P16170 xenopus lae
2	234.5	13.3	515	PVAL_PIG	O99176 sus scrofa
3	227.5	12.9	517	PVAL_HUMAN	O15223 homo sapien
4	224	12.7	530	PVAL_MOUSE	P32507 mus musculu
5	223.5	12.7	837	NCM2_MOUSE	O35136 mus musculu
6	223	12.7	1092	NCAM2_XENLA	P36335 xenopus lae
7	222	12.6	344	NTRI_RAT	O62718 rattus norv
8	221	12.5	417	PVR_CERAE	P32506 cercopithe
9	221	12.5	538	PVAL_HUMAN	O92692 homo sapien
10	219	12.4	337	G55A_CHICK	O98892 gallus gall
11	217	12.3	417	PVR_HUMAN	P15151 homo sapien
12	214.5	12.2	837	NCM2_HUMAN	O15394 homo sapien
13	213	12.0	4393	PGHM_HUMAN	P98160 homo sapien
14	210.5	12.0	345	OPCM_BOVIN	P11834 bos taurus
15	210	11.9	1242	OPCM_MOUSE	O94257 mus musculu
16	208.5	11.8	345	OPCM_HUMAN	O14982 homo sapien
17	208	11.8	515	PVAL_MOUSE	O91Kf6 mus musculu
18	208	11.8	1493	NEOL_MOUSE	P93798 mus musculu
19	207	11.8	847	CD22_HUMAN	P20273 homo sapien
20	206	11.7	702	CEAS_HUMAN	P06731 homo sapien
21	203	11.5	1461	NEOL_HUMAN	O92859 homo sapien
22	202.5	11.5	345	OPCM_RAT	P32736 rattus norv
23	202.5	11.5	353	CEPU_CHICK	O90773 gallus gall
24	203.5	11.5	862	CD22_MOUSE	P35329 mus musculu
25	202	11.5	1377	NEOL_RAT	P97603 rattus norv
26	197.5	11.1	1443	NEOL_CHICK	O90610 gallus gall
27	197.5	11.1	3707	PGHM_MOUSE	O05793 mus musculu
28	195.5	11.1	1091	NCAL_CHICK	P13590 gallus gall
29	195.5	11.1	1234	NPHN_RAT	O91040 rattus norv
30	195	11.0	583	CL66_MOUSE	O61490 mus musculu
31	194	11.0	388	LAMP_CHICK	O98519 gallus gall
32	193	11.0	761	NCAM2_HUMAN	P13592 homo sapien
33	193	11.0	848	NCAL_HUMAN	P13591 homo sapien

34	192.5	10.9	1241	1	NPHN_HUMAN	O60500 homo sapien
35	190	10.8	1447	1	DCC_MOUSE	P70211 mus musculu
36	189.5	10.8	646	1	MU18_HUMAN	P43121 homo sapien
37	189	10.7	1036	1	AXOL_CHICK	P28685 gallus gall
38	188.5	10.7	764	1	ICCR_DROME	O08180 drosophila
39	188	10.7	853	1	NCAL_BOVIN	P31836 bos taurus
40	188	10.7	858	1	NCAL_RAT	P13596 rattus norv
41	187.5	10.6	583	1	CL66_HUMAN	O13740 homo sapien
42	187	10.6	588	1	CL66_CHICK	P42292 gallus gall
43	185.5	10.5	338	1	LAMP_HUMAN	O13449 homo sapien
44	183.5	10.4	338	1	LAMP_RAT	O62813 rattus norv
45	182.5	10.4	873	1	FAS2_DROME	P34082 drosophila

ALIGNMENTS

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RESULT 1
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DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
DE 180).
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90098871; PubMed=2481269;
RA Kriegl P.A., Sakaguchi D.S., Kintner C.R.;
RT "Primary structure and developmental expression of a large
RT cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT molecule (NCAM)".
RL Nucleic Acids Res. 17:10321-10335(1989).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC -1- NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC -1- NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: N-CAM 180 (shown here) and
CC -1- N-CAM 140; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC -1- TISSUE.
CC -1- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC -1- TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC -1- EARLY NEURAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC -1- between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC -1- the European Bioinformatics Institute. There are no restrictions on its
CC -1- use by non-profit institutions as long as its content is in no way
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CC -1- entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC -1- or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M25696; AAA49909.1; -
DR PIR: S09600; IJXJNL.
DR HSP: P56276; IYK.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003598; IG_C2.
DR Pfam: PF00041; FN3; 2.
DR Pfam: PF00047; IG; 5.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00408; IGC2; 5.

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KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW Immunoglobulin domain; Alternative splicing; Signal.
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FT CHAIN 20 1088
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1088
FT DOMAIN 134 100
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FT DOMAIN 316 386
FT DOMAIN 415 480
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FT CARBOHYD 82 82
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SQ SEQUENCE 1088 AA; 117778 MW; 6273855B03F3E83 CRC64;

Query Match 13.6%; Score 239; DB 1; Length 1088;
Best Local Similarity 26.2%; Pred. No. 3.4e-10;
Matches 89; Conservative 62; Mismatches 147; Indels 42; Gaps 15;

QY 12 KDVTYVEGAVATISCC---OVNKS---DDSVYQLN---PNKQTYFRDPLKDSRFOL 61
DB 199 KDIQVYVNPPTIOARQLRNATNANNAESVYLSCDADGFPDPETISWLKKEPIEDGE-EK 257
QY 62 LNFSSSEKLSTNVSISDGRYFCOLYTPDQESYTYTIVLPPRLMLDICKDRAVEG 121
DB 258 ISNNEQSEKTIHVEKDEAEISC--IANNQGEAEKTIILKAYAKPKITYENKRAVEL 316
QY 122 EELVNCNTAMASKPATTIRN-----FKGNETLKSKSEYEEMSDYTVTSQMLKYHKE 174
DB 317 DETLTCEA-SGDPISPTWRTAVRNISSEATLDDGHIVYKHEIRM---SALTLDIOY 371
QY 175 DDCVPYICQVEHNAVGNQOTQRYLEVQKRPQYHIQMTYPLQGLTRBGDALELTCEALIK 234
DB 372 TDGGEYFCIASNP-IGVDQAM-YFEVQYAPKIR---GAVVYVYTWEGMNVNTICEVFAH 425
QY 235 POFVATVYVVDDEMPQH-----AVLSGP---NLAFINLNKTDNGTYRCFASNTYKASH 286
DB 426 PR-AATWTRDGLLPSSNSNKIKYSGPTSSSLEVNPPSEDPFGNCAINTIGHEFS 484
QY 287 DYMLVYVDPPTTTPPTTT 326
DB 485 EFLIVQADTPSS---PAIRKVEPYSVTMIVFEDPDSTG 521

RESULT 2
PVARL_PIG STANDARD; PRT; 515 AA.
AC 09GL76;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvC) (Nectin 1).
GN PVARL OR PRL OR HVCC.
OS Sus srofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krümmenacher C., Eisenberg R.J., Cohen G.H.;
RT "Porcine HvC, a member of the highly conserved HvC/nectin 1 family, is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
CC -1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF08632; AAG30281.1; -
DR HSSP; P06907; INEU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PR00047; Ig_2.
DR SMART; SM00409; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00408; ICG2; 2.
DR SMART; SM00406; IGV; 1.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 305
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT DOMAIN 44 131
FT DOMAIN 165 233
FT DOMAIN 262 323
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
SQ SEQUENCE 515 AA; 57047 MW; BFA800320DDE3785 CRC64;

Query Match 13.3%; Score 234.5; DB 1; Length 515;
Best Local Similarity 25.7%; Pred. No. 2.8e-10;
Matches 80; Conservative 50; Mismatches 130; Indels 51; Gaps 12;

QY 14 VYVEGEVATISQVANKSDSVYQLNPNKQTYFRDPLKDSRFOLNFSSELKVS 73
DB 62 INQVYVQKATNGSKN-----VAIYNPAMGVSVALPYR-----ERAEPLRPSTDTGTR 111
QY 74 TNVVISDEGRYFCQLYTDPP--QESYTTITVLPVPRNMLDIO-----KDTAVEGEE 123


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1  PRIOR APPLICATION NUMBER: 60/069,702
2  PRIOR FILING DATE: December 16, 1997
3  PRIOR APPLICATION NUMBER: 60/069,870
4  PRIOR FILING DATE: December 17, 1997
5  PRIOR APPLICATION NUMBER: 60/069,873
6  PRIOR FILING DATE: December 17, 1997
7  PRIOR APPLICATION NUMBER: 60/068,017
8  PRIOR FILING DATE: December 18, 1997
9  PRIOR APPLICATION NUMBER: 60/070,440
10 PRIOR FILING DATE: January 5, 1998
11 PRIOR APPLICATION NUMBER: 60/074,086
12 PRIOR FILING DATE: February 9, 1998
13 PRIOR APPLICATION NUMBER: 60/074,092
14 PRIOR FILING DATE: February 9, 1998
15 PRIOR APPLICATION NUMBER: 60/075,945
16 PRIOR FILING DATE: February 25, 1998
17 PRIOR APPLICATION NUMBER: 60/112,850
18 PRIOR FILING DATE: December 16, 1998
19 PRIOR APPLICATION NUMBER: 60/113,296
20 PRIOR FILING DATE: December 22, 1998
21 PRIOR APPLICATION NUMBER: 60/146,222
22 PRIOR FILING DATE: July 28, 1999
23 PRIOR APPLICATION NUMBER: PCT/US98/19330
24 PRIOR FILING DATE: September 16, 1998
25 PRIOR APPLICATION NUMBER: PCT/US98/25108
26 PRIOR FILING DATE: December 1, 1998
27 PRIOR APPLICATION NUMBER: 09/216,021
28 PRIOR FILING DATE: December 16, 1998
29 PRIOR APPLICATION NUMBER: 09/218,517
30 PRIOR FILING DATE: December 22, 1998
31 PRIOR APPLICATION NUMBER: 09/254,311
32 PRIOR FILING DATE: March 3, 1999
33 PRIOR APPLICATION NUMBER: PCT/US99/12252
34 PRIOR FILING DATE: June 22, 1999
35 PRIOR APPLICATION NUMBER: PCT/US99/21090
36 PRIOR FILING DATE: September 15, 1999
37 PRIOR APPLICATION NUMBER: PCT/US99/28409
38 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
39 PRIOR APPLICATION NUMBER: PCT/US99/28313
40 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
41 PRIOR APPLICATION NUMBER: PCT/US99/28301
42 PRIOR FILING DATE: December1, 1999
43 PRIOR APPLICATION NUMBER: PCT/US99/30095
44 PRIOR FILING DATE: December 16, 1999
45 PRIOR APPLICATION NUMBER: PCT/US00/03565
46 PRIOR FILING DATE: February 11, 2000
47 PRIOR APPLICATION NUMBER: PCT/US00/04414
48 PRIOR FILING DATE: February 22, 2000
49 PRIOR APPLICATION NUMBER: PCT/US00/05841
50 PRIOR FILING DATE: March 2, 2000
51 PRIOR APPLICATION NUMBER: PCT/US00/08439
52 PRIOR FILING DATE: March 30, 2000
53 PRIOR APPLICATION NUMBER: PCT/US00/14042
54 PRIOR FILING DATE: May 22, 2000
55 PRIOR APPLICATION NUMBER: PCT/US00/20710
56 PRIOR FILING DATE: July 28, 2000
57 PRIOR APPLICATION NUMBER: PCT/US00/32678
58 PRIOR FILING DATE: December 1, 2000
59 PRIOR APPLICATION NUMBER: PCT/US01/06520
60 PRIOR FILING DATE: February 28, 2001
61 NUMBER OF SEQ ID NOS: 120
62 SEQ ID NO 61
63 LENGTH: 440
64 TYPE: PRT
65 ORGANISM: Homo Saplen
66 US-09-944-413-61

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Query Match          100.0%; Score 1761; DB 9; Length 440;
Best Local Similarity 100.0%; Pred. No. 1,7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y      1 IPTGGGQNLFFRDVAVIGGEVATISGVNKKSDSDSYIQLNPNKQITTFEDFERPLKDSRFQ 60
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D	b	37	IPRGGQGLFFRKDVTVIEGEVAATISCGYKNSDSDVQLDLMNRRQITIEFRFRPLKDSRFQ	96
O	y	61	LNINSSSELKAKSLINWVSIISDGRFCQJLYDTPROESTTTIVLVPYRNIMIDIOKDTAVE	120
D	b	97	LNINSSSELKAKSLINWVSIISDGRFCQJLYDTPROESTTTIVLVPYRNIMIDIOKDTAVE	156
O	y	121	GEIEEVNCTAASKRPAITIRMFKNKNTLKGSEVEEWSMDTVYSQMLVKVHKEDDQVY	180
D	b	157	GEIEEVNCTAASKRPAITIRMFKNKNTLKGSEVEEWSMDTVYSQMLVKVHKEDDQVY	216
O	y	181	ICQVHNRAVNTLOQRYLEVOYKPOVNIQMTYLOGLTREGALLETLSAIGKPOVWY	240
D	b	217	ICQVHNRAVNTLOQRYLEVOYKPOVNIQMTYLOGLTREGALLETLSAIGKPOVWY	276
O	y	241	TWVRVDDMPQHAVALSGENLEINMLNKNTDNGTCSEASINVGAKSHSDYMLVYDPRPTIP	300
D	b	277	TWVRVDDMPQHAVALSGENLEINMLNKNTDNGTCSEASINVGAKSHSDYMLVYDPRPTIP	336
O	y	301	PRTPTTTTTTTTTTTTTLITLINDSRAGEGSRAYDH	336
D	b	337	PRTPTTTTTTTTTTTTTLITLINDSRAGEGSRAYDH	372

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RESULT 2
US-09-944-403-61
: Sequence 61. Application US/09944403
: Patent No. US20020165143A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavins, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OR INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,403
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997

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: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-944-403-61

Query Match      100.0%: Score 1761: DB 9: Length 440:
Best Local Similarity 100.0%: Pred. No. 1.7e-105:
Matches 336: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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Db      157  GEEIEVNCAMASKPATTTIRMGKNTLGKSEVEEWSDMYTTYSQMLMKVHKEDGCVY 216
Qy      181  ICQVEHPAVTGNLTQRYLEVOYKPPQVHIQMTYPIQGLTREGDALELTCEAIKPPQVW 240
Db      217  ICQVEHPAVTGNLTQRYLEVOYKPPQVHIQMTYPIQGLTREGDALELTCEAIKPPQVW 276
Qy      241  TWVRVDEMPQNAVISGPNLFTNNLKNKTNDNGTYRCASNVGKAHSDYMLYVDPPTTIP 300
Db      277  TWVRVDEMPQNAVISGPNLFTNNLKNKTNDNGTYRCASNVGKAHSDYMLYVDPPTTIP 336
Qy      301  PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 336
Db      337  PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 372

RESULT 3
US-09-944-896-61
: Sequence 61, Application US/09944896
: Patent No. US20020168715A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548PICI
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: US/09/944,896
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998

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; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-896-61

Query Match      100.0%; Score 1761; DB 9; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IPTGDDGNLFTKDVYIEGEVATISCOVKNKSDSVIQLNPNKQTYFRDPRFLKDSRFQ 60
DB 37 IPTGDDGNLFTKDVYIEGEVATISCOVKNKSDSVIQLNPNKQTYFRDPRFLKDSRFQ 96
QY 61 LNFSSSELKVSLLTNVISDEGRYFCOLYTDPPQESTTTTIVLPPRNLMIDIOKDTAVE 120
DB 97 LNFSSSELKVSLLTNVISDEGRYFCOLYTDPPQESTTTTIVLPPRNLMIDIOKDTAVE 156
QY 121 GEEIEVNCSTAMASKPATTTIRFWKNTLKGKSEVEEMSDMYTTSOLMLKVHKEDGVPV 180
DB 157 GEEIEVNCSTAMASKPATTTIRFWKNTLKGKSEVEEMSDMYTTSOLMLKVHKEDGVPV 216
QY 181 ICQVEHPAYTGNLQOTORYLEVQYKRPVHIQMTYPLQGLTFREGDALELTCEAIKQPVMV 240
DB 217 ICQVEHPAYTGNLQOTORYLEVQYKRPVHIQMTYPLQGLTFREGDALELTCEAIKQPVMV 276
QY 241 TWVRVDDEMPQAHVLSGPNLFINNLTNGTYRCEASNTVGAHSDYMLYVDPPTTIP 300
DB 277 TWVRVDDEMPQAHVLSGPNLFINNLTNGTYRCEASNTVGAHSDYMLYVDPPTTIP 336
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QY 301 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKRAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKRAVDH 372
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RESULT 4
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bolstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match      100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IPTGDDGNLFTKDVYIEGEVATISCOVKNKSDSVIQLNPNKQTYFRDPRFLKDSRFQ 60
DB 37 IPTGDDGNLFTKDVYIEGEVATISCOVKNKSDSVIQLNPNKQTYFRDPRFLKDSRFQ 96
QY 61 LNFSSSELKVSLLTNVISDEGRYFCOLYTDPPQESTTTTIVLPPRNLMIDIOKDTAVE 120
DB 97 LNFSSSELKVSLLTNVISDEGRYFCOLYTDPPQESTTTTIVLPPRNLMIDIOKDTAVE 156
QY 121 GEEIEVNCSTAMASKPATTTIRFWKNTLKGKSEVEEMSDMYTTSOLMLKVHKEDGVPV 180
DB 157 GEEIEVNCSTAMASKPATTTIRFWKNTLKGKSEVEEMSDMYTTSOLMLKVHKEDGVPV 216
QY 181 ICQVEHPAYTGNLQOTORYLEVQYKRPVHIQMTYPLQGLTFREGDALELTCEAIKQPVMV 240
DB 217 ICQVEHPAYTGNLQOTORYLEVQYKRPVHIQMTYPLQGLTFREGDALELTCEAIKQPVMV 276
QY 241 TWVRVDDEMPQAHVLSGPNLFINNLTNGTYRCEASNTVGAHSDYMLYVDPPTTIP 300
DB 277 TWVRVDDEMPQAHVLSGPNLFINNLTNGTYRCEASNTVGAHSDYMLYVDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKRAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKRAVDH 372

RESULT 5
US-09-944-449-61
; Sequence 61, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Flvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 5, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-449-61
Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IPGGDQNLFTKDYVYIEGEVATISCVNKSDDSVIQLNPNKOTYFRDFRLKSRQ 60
DB 37 IPGGDQNLFTKDYVYIEGEVATISCVNKSDDSVIQLNPNKOTYFRDFRLKSRQ 96
QY 61 LNFSSSELKVSILTNVISDEGRFCOLYTDPPQESYTTTYVVPRLNMLIDOKTAVE 120
DB 97 LNFSSSELKVSILTNVISDEGRFCOLYTDPPQESYTTTYVVPRLNMLIDOKTAVE 156
QY 121 GEEIEVNCATAMASKPATTTTTFKNTLKGSEVEEMSDMTVTTSQMLKVKHEDGVPV 180
DB 157 GEEIEVNCATAMASKPATTTTTFKNTLKGSEVEEMSDMTVTTSQMLKVKHEDGVPV 216
QY 181 ICQVEHPAVTGNLQIOTRYLEVOYKPOVHIOMTYPLDGLTREGDALELTCEAIGKPPVNV 240
DB 217 ICQVEHPAVTGNLQIOTRYLEVOYKPOVHIOMTYPLDGLTREGDALELTCEAIGKPPVNV 276
QY 241 TWVRVDEMPQAHAVLSGPNLFTNNLKTNGTYRCEASNIVGKAHSDMYLYVDPPTTIP 300
DB 277 TWVRVDEMPQAHAVLSGPNLFTNNLKTNGTYRCEASNIVGKAHSDMYLYVDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTTTTTTIDSRAGEEGSIRAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTIDSRAGEEGSIRAVDH 372
RESULT 6
US-09-944-457-61
Sequence 61, Application US/09944457
Patent No. US20020110859A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Flvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/03841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-61
Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IPFGDGNLFTKDVTEGEVATISCOVNSDSVIOLLNPNQTYFRDPRPKDSRFQ 60
DB 37 IPFGDGNLFTKDVTEGEVATISCOVNSDSVIOLLNPNQTYFRDPRPKDSRFQ 96
QY 61 LNFSSSELKVSLSLTVSISDEGRFCQLYNDPPESTYTTTVLVPNNLMIDIOKDAVE 120
DB 97 LNFSSSELKVSLSLTVSISDEGRFCQLYNDPPESTYTTTVLVPNNLMIDIOKDAVE 156
QY 121 GEEIEVNCCTAMASKPATTTIMFKGNTELKKGSEVEESDMYTYTSQMLKVHKEDGVPV 180
DB 157 GEEIEVNCCTAMASKPATTTIMFKGNTELKKGSEVEESDMYTYTSQMLKVHKEDGVPV 216
QY 181 ICQVHPAVGNLQTOYKYLVOYKPOVHTQMTYPLQSLTREGALLETCAIGKPOVNV 240
DB 217 ICQVHPAVGNLQTOYKYLVOYKPOVHTQMTYPLQSLTREGALLETCAIGKPOVNV 276
QY 241 TWVRVDEMPQHVAVLSGPNLFNNLNKTDNGTYRCEASNVGKASDYMLYVVDPPPTIP 300
DB 277 TWVRVDEMPQHVAVLSGPNLFNNLNKTDNGTYRCEASNVGKASDYMLYVVDPPPTIP 336
QY 301 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKRAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKRAVDH 372
RESULT 7
US-09-944-862-61
Sequence 61, Application US/09944862
Patent No. US20020115145A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William


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1  TITLE OR INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEI
2  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
3  FILE REFERENCE:  p2548pic1
4  CURRENT APPLICATION NUMBER:  US/09/944,862
5  PRIOR FILING DATE:  2001-09-26
6  PRIOR APPLICATION NUMBER:  09/866,028
7  PRIOR FILING DATE:  2001-05-25
8  PRIOR APPLICATION NUMBER:  60/067,411
9  PRIOR FILING DATE:  December 3, 1997
10 PRIOR APPLICATION NUMBER:  60/069,334
11 PRIOR FILING DATE:  December 11, 1997
12 PRIOR APPLICATION NUMBER:  60/069,335
13 PRIOR FILING DATE:  December 11, 1997
14 PRIOR APPLICATION NUMBER:  60/069,278
15 PRIOR FILING DATE:  December 11, 1997
16 PRIOR APPLICATION NUMBER:  60/069,425
17 PRIOR FILING DATE:  December 12, 1997
18 PRIOR APPLICATION NUMBER:  60/069,696
19 PRIOR FILING DATE:  December 16, 1997
20 PRIOR APPLICATION NUMBER:  60/069,694
21 PRIOR FILING DATE:  December 16, 1997
22 PRIOR APPLICATION NUMBER:  60/069,702
23 PRIOR FILING DATE:  December 16, 1997
24 PRIOR APPLICATION NUMBER:  60/069,870
25 PRIOR FILING DATE:  December 17, 1997
26 PRIOR APPLICATION NUMBER:  60/069,873
27 PRIOR FILING DATE:  December 17, 1997
28 PRIOR APPLICATION NUMBER:  60/068,017
29 PRIOR FILING DATE:  December 18, 1997
30 PRIOR APPLICATION NUMBER:  60/070,440
31 PRIOR FILING DATE:  January 5, 1998
32 PRIOR APPLICATION NUMBER:  60/074,086
33 PRIOR FILING DATE:  February 9, 1998
34 PRIOR APPLICATION NUMBER:  60/074,092
35 PRIOR FILING DATE:  February 9, 1998
36 PRIOR APPLICATION NUMBER:  60/075,945
37 PRIOR FILING DATE:  February 25, 1998
38 PRIOR APPLICATION NUMBER:  60/112,850
39 PRIOR FILING DATE:  December 16, 1998
40 PRIOR APPLICATION NUMBER:  60/113,296
41 PRIOR FILING DATE:  December 22, 1998
42 PRIOR APPLICATION NUMBER:  60/146,222
43 PRIOR FILING DATE:  July 28, 1999
44 PRIOR APPLICATION NUMBER:  PCT/US99/19330
45 PRIOR FILING DATE:  September 16, 1998
46 PRIOR APPLICATION NUMBER:  PCT/US99/25108
47 PRIOR FILING DATE:  December 1, 1998
48 PRIOR APPLICATION NUMBER:  09/216,021
49 PRIOR FILING DATE:  December 16, 1998
50 PRIOR APPLICATION NUMBER:  09/218,517
51 PRIOR FILING DATE:  December 22, 1998
52 PRIOR APPLICATION NUMBER:  09/254,311
53 PRIOR FILING DATE:  March 3, 1999
54 PRIOR APPLICATION NUMBER:  PCT/US99/12252
55 PRIOR FILING DATE:  June 22, 1999
56 PRIOR APPLICATION NUMBER:  PCT/US99/21090
57 PRIOR FILING DATE:  September 15, 1999
58 PRIOR APPLICATION NUMBER:  PCT/US99/28409
59 PRIOR FILING DATE:  NO. US20020115145A1member 30, 1999
60 PRIOR APPLICATION NUMBER:  PCT/US99/28313
61 PRIOR FILING DATE:  NO. US20020115145A1member 30, 1999
62 PRIOR APPLICATION NUMBER:  PCT/US99/28301
63 PRIOR FILING DATE:  December 1, 1999
64 PRIOR APPLICATION NUMBER:  PCT/US99/30095
65 PRIOR FILING DATE:  December 16, 1999
66 PRIOR APPLICATION NUMBER:  PCT/US00/03565
67 PRIOR FILING DATE:  February 11, 2000
68 PRIOR APPLICATION NUMBER:  PCT/US00/04414
69 PRIOR FILING DATE:  February 22, 2000
70 PRIOR APPLICATION NUMBER:  PCT/US00/05841
71 PRIOR FILING DATE:  March 2, 2000
72 PRIOR APPLICATION NUMBER:  PCT/US00/08439
73 PRIOR FILING DATE:  March 30, 2000

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1  PRIOR APPLICATION NUMBER: PCT/US00/14042
2  PRIOR FILING DATE: May 22, 2000
3  PRIOR APPLICATION NUMBER: PCT/US00/20710
4  PRIOR FILING DATE: July 28, 2000
5  PRIOR APPLICATION NUMBER: PCT/US00/32678
6  PRIOR FILING DATE: December 1, 2000
7  PRIOR APPLICATION NUMBER: PCT/US01/06520
8  PRIOR FILING DATE: February 28, 2001
9  NUMBER OF SEQ ID NOS: 120
10
11 SEQ ID NO 61
12 LENGTH: 440
13 TYPE: PRT
14 ORGANISM: Homo Sapien
15 US-09-944-862-61
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17 Query Match 100.0%; Score 1761; DB 10; Length 440;
18 Best Local Similarity 100.0%; Pred. No. 1,7e-105;
19 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20
21 QY 1 IPTGGQNLFRKDVYVIEGEVATISCVNKKSDSVYQLNPNRQTIYRDRPRLKDSRFQ 60
22 Db 37 IPTGGQNLFRKDVYVIEGEVATISCVNKKSDSVYQLNPNRQTIYRDRPRLKDSRFQ 96
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24 QY 61 LFNSSSELKAVSLTNVSTSDRGRTFCQLYTDPRQESYTTITVLVPPNLMIDIQKTAVE 120
25 Db 97 LFNSSSELKAVSLTNVSTSDRGRTFCQLYTDPRQESYTTITVLVPPNLMIDIQKTAVE 156
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27 QY 121 GEEIEVNTAAASKRATITIRNFKGTTELKGSSEVEEMSDMTVTNLSQLMKVHKEDDGPV 180
28 Db 157 GEEIEVNTAAASKRATITIRNFKGTTELKGSSEVEEMSDMTVTNLSQLMKVHKEDDGPV 216
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30 QY 181 ICQVEHPAVTGNLQTRYLEVOYKQVHIQMTYPLQGLTREGDALLETCEAIGKQPVMV 240
31 Db 217 ICQVEHPAVTGNLQTRYLEVOYKQVHIQMTYPLQGLTREGDALLETCEAIGKQPVMV 276
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33 QY 241 TWVRVDDMPQHAYLSGNLFTNNLNKTDNGTYRCEASNIYGAKASDMLVYDPPPTIP 300
34 Db 277 TWVRVDDMPQHAYLSGNLFTNNLNKTDNGTYRCEASNIYGAKASDMLVYDPPPTIP 336
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36 QY 301 PPTTTTTTTTTTTTTLTIITDSRAGEGSGIRAVDH 336
37 Db 337 PPTTTTTTTTTTTTTLTIITDSRAGEGSGIRAVDH 372
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39 RESULT 8
40 US-09-945-587-61
41 Sequence 61, Application us/09945587
42 Patent No. US20020127643A1
43 GENERAL INFORMATION:
44 APPLICANT: Baker, Kevin
45 APPLICANT: Batstein, David
46 APPLICANT: Eaton, Dan
47 APPLICANT: Ferrara, Napoleone
48 APPLICANT: Filvaroff, Ellen
49 APPLICANT: Gerritsen, Mary
50 APPLICANT: Goddard, Audrey
51 APPLICANT: Godowski, Paul
52 APPLICANT: Grimaldi, Christopher
53 APPLICANT: Gurney, Austin
54 APPLICANT: Hillan, Kenneth
55 APPLICANT: Kljavin, Ivar
56 APPLICANT: Napier, Mary
57 APPLICANT: Roy, Margaret
58 APPLICANT: Tumas, Daniel
59 APPLICANT: Wood, William
60 TITLE OF INVENTION: SCRYPTED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
61 FILE REFERENCE: P2548P1C1
62 CURRENT APPLICATION NUMBER: US/09/945, 587
63 PRIOR APPLICATION NUMBER: 09/866, 028
64 PRIOR FILING DATE: 2001-05-25
65 PRIOR APPLICATION NUMBER: 60/067,411

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PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,596
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020127643A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US20020127643A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001

NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-945-587-61
Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1,7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IPTDGGNLFTRKDVTVIEGEVATISQVYKSDSVIQLLNPNROTIFYRDRPLKDSRFQ 60
DB 37 IPTDGGNLFTRKDVTVIEGEVATISQVYKSDSVIQLLNPNROTIFYRDRPLKDSRFQ 96
QY 61 LLNSSFLLKSLTLNVSTSDGRCFQLYTPDPESTTTTVLVPRLMIDIKDTAVE 120
DB 97 LLNSSFLLKSLTLNVSTSDGRCFQLYTPDPESTTTTVLVPRLMIDIKDTAVE 156
QY 121 GEEIEVNCTAMASKPATIRFNGNTELGKSEVEEMSDMTYTSOLMLKYHKEDGVPV 180
DB 157 GEEIEVNCTAMASKPATIRFNGNTELGKSEVEEMSDMTYTSOLMLKYHKEDGVPV 216
QY 181 ICQVHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQGLTRGDALELTCEAIKRPQPMV 240
DB 217 ICQVHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQGLTRGDALELTCEAIKRPQPMV 276
QY 241 TWAVVDEDMQHAVLSGPNLFNNLNTDNGTYCEASNIYGRKHSYMLYVDPPTTIP 300
DB 277 TWAVVDEDMQHAVLSGPNLFNNLNTDNGTYCEASNIYGRKHSYMLYVDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTLTIITDSRAGEGSIRAVDH 336
DB 337 PPTTTTTTTTTTTTTLTIITDSRAGEGSIRAVDH 372
RESULT 9
US-09-945-015-61
Sequence 61, Application us/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945, 015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425

PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/234,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Saplen
US-09-945-015-61

Query Match 100.0%; Score 1761; DB 10; Length 440;

Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IPGDDONLFTKDVYIEBEVATISCOVKNKSDSVIOLLNPNKOTYFNRFRLLKNSRFQ 60
Db 37 IPGDDONLFTKDVYIEBEVATISCOVKNKSDSVIOLLNPNKOTYFNRFRLLKNSRFQ 96
QY 61 LNFSSSELKVSLLTVNSISDEGRFCOLYTDPPQESYTTTVLVPPRLMIDIOKTAVE 120
Db 97 LNFSSSELKVSLLTVNSISDEGRFCOLYTDPPQESYTTTVLVPPRLMIDIOKTAVE 156
QY 121 GEIEVNCNTAMASKPATYTRWFKGNTLKGKSEVEEWSMDYTVTSOLMLKVHKEDGCVY 180
Db 157 GEIEVNCNTAMASKPATYTRWFKGNTLKGKSEVEEWSMDYTVTSOLMLKVHKEDGCVY 216
QY 181 ICQVHPAVTGNLQOTRYLEVOYKPOVHIOMYPLQGLTREGDALLTCEALGKPOVWV 240
Db 217 ICQVHPAVTGNLQOTRYLEVOYKPOVHIOMYPLQGLTREGDALLTCEALGKPOVWV 276
QY 241 TWVRVDENPOHVALSGPNLFNNLNKTDNGTYRCEASNIYGAHSDMYLVYDPPPTTP 300
Db 277 TWVRVDENPOHVALSGPNLFNNLNKTDNGTYRCEASNIYGAHSDMYLVYDPPPTTP 336
QY 301 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKAVDH 336
Db 337 PPTTTTTTTTTTTTTTTTTTDSRAGEGSIKAVDH 372
RESULT 10
US-09-944-396-61
Sequence 61, Application US/09944396
Patent No. US20020132981A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/944,396
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870

;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020132981A member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020132981A member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-396-61

Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPTGDCQNTFTKDVYIEGEVATISCOVNSDSDSVIQLNPNQOTYFRDPRFKLSRFQ 60
Db 37 IPTGDCQNTFTKDVYIEGEVATISCOVNSDSDSVIQLNPNQOTYFRDPRFKLSRFQ 96
Qy 61 LNFSSSELKSVLTNVSISDEGRYFCQLYTPDPEESYTTITVLVPPRNLMIDIOKDTAVE 120

Db 97 LNFSSSELKSVLTNVSISDEGRYFCQLYTPDPEESYTTITVLVPPRNLMIDIOKDTAVE 156
Qy 121 GEELFVNCSTMAKSPATTIRFKNTFLKSGSEVEBSMDWTYTSOLMLKVKHKKDDCPV 180
Db 157 GEELFVNCSTMAKSPATTIRFKNTFLKSGSEVEBSMDWTYTSOLMLKVKHKKDDCPV 216
Qy 181 ICQYENPAVTGNLOTOYKYLEVQKPYHIOMTYPLQGLTREGDALLETCEAIGKPPVMV 240
Db 217 ICQYENPAVTGNLOTOYKYLEVQKPYHIOMTYPLQGLTREGDALLETCEAIGKPPVMV 276
Qy 241 TWVRVDEMPQHAVLSCPNLEFINNLKNTDNGYRCEASNIYKAHSDYMLVYDPTTIP 300
Db 277 TWVRVDEMPQHAVLSCPNLEFINNLKNTDNGYRCEASNIYKAHSDYMLVYDPTTIP 336
Qy 301 PPTTTTTTTTTTTTTTTTTTSDRAGEGSTRADVH 336
Db 337 PPTTTTTTTTTTTTTTTTTTSDRAGEGSTRADVH 372

RESULT 11
US-09-944-097-61

;; Sequence 61, Application US/09944097
;; Patent No. US2002013675A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerlitsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kijavlin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/944,097
;; CURRENT FILING DATE: 2001-08-31
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020133675A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020133675A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-097-61

Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IPFGDQNLFTADYVIEGEVATISCVNKSQSDSVIQLPNKQTYFRDRLKDSRFQ 60
|||||
37 IPFGDQNLFTADYVIEGEVATISCVNKSQSDSVIQLPNKQTYFRDRLKDSRFQ 96
|||||
61 LNFSSSELKSVLTNVSIDEGRYFCOLYTDPPQESTYTTTVVPPRNLMIDIOKTAVE 120
|||||
97 LNFSSSELKSVLTNVSIDEGRYFCOLYTDPPQESTYTTTVVPPRNLMIDIOKTAVE 156
|||||
121 GEEIEVNCAMASKPATITRMFGNTELGKSEVEEEMSDMYTYSQMLKVKHEDGCPV 180
|||||
157 GEEIEVNCAMASKPATITRMFGNTELGKSEVEEEMSDMYTYSQMLKVKHEDGCPV 216
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181 IGOVEHPATYGNLQOTRYLEVQYKRPVNHQMTYPLQGLTREGALLETGCAIKPQPVWY 240
|||||
217 IGOVEHPATYGNLQOTRYLEVQYKRPVNHQMTYPLQGLTREGALLETGCAIKPQPVWY 276
|||||

241 TWRVDEMPQAHAVLSGPNLFINNLTNGTYRCEASNIVGKAHSDMYLVYDPPPTIP 300
|||||
277 TWRVDEMPQAHAVLSGPNLFINNLTNGTYRCEASNIVGKAHSDMYLVYDPPPTIP 336
|||||
301 PPTTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDH 336
|||||
337 PPTTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDH 372
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RESULT 12

US-09-944-432-61
Sequence 61, Application US/09944432
Patent No. US20020142419A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Guiney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kjaevlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222

;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: NO. US20020142419A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: NO. US20020142419A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-432-61

Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGDSQNLFTKDVVIEGEVATISCOVNSKSDSVIQLNPNKQIYFRDPRFLKDSRFQ 60
DB 37 IPTGDSQNLFTKDVVIEGEVATISCOVNSKSDSVIQLNPNKQIYFRDPRFLKDSRFQ 96

QY 61 LNFSSSELKSVLTNVSISSEGRYFCQLYTDPPQESYTTITVLPVPRNLMDIOKDTAVE 120
DB 97 LNFSSSELKSVLTNVSISSEGRYFCQLYTDPPQESYTTITVLPVPRNLMDIOKDTAVE 156

QY 121 GEEIEVNCATAMASKPATTTIKMFKGNTELKGSSEVEESMDXYTWSOLMLKVNKEDGCVPV 180
DB 157 GEEIEVNCATAMASKPATTTIKMFKGNTELKGSSEVEESMDXYTWSOLMLKVNKEDGCVPV 216

QY 181 ICQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLREGDALELTCEAIKPPQVMV 240
DB 217 ICQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLREGDALELTCEAIKPPQVMV 276

QY 241 TWVRVVDENPQAHVLSGPNLFINNLKKTNGTIRCAASNVGCAHSDYMLVYVDPPTTIP 300
DB 277 TWVRVVDENPQAHVLSGPNLFINNLKKTNGTIRCAASNVGCAHSDYMLVYVDPPTTIP 336

QY 301 PPTTTTTTTTTTTTTTTTTTSSRAGEEGSIRAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTSSRAGEEGSIRAVDH 372

RESULT 13
US-09-943-762-61
; Sequence 61, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: KJavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/943,762
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517

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: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-943-762-61

Query Match      100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1,7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 37 IPTGGQNLFTRDVYIEGEVATISQVVKSDSVIQLLNPNRQTIYFRDPRLKDNRQ 96
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QY 181 IGOVEHPAVTGNLQTRYLEVOYKPPQVHIQMTYPLQGLTREGDALELTCEAIGKPPQVW 240
DB 217 IGOVEHPAVTGNLQTRYLEVOYKPPQVHIQMTYPLQGLTREGDALELTCEAIGKPPQVW 276
QY 241 TTVRRVDDDEHPQAHVLSGPNLFTNNLKNKTNGTYRCASNIYVGAHSDYMLYYVDPTTTP 300
DB 277 TTVRRVDDDEHPQAHVLSGPNLFTNNLKNKTNGTYRCASNIYVGAHSDYMLYYVDPTTTP 336
QY 301 PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 336
DB 337 PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 372

RESULT 14
US-09-944-654-61
: Sequence 61, Application US/09944654
: Patent No. US20020142959A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
```

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: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548PICI
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
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: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
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: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
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: PRIOR APPLICATION NUMBER: 60/113,296
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: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
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;; PRIOR FILING DATE: No. US20020142959a1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020142959a1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-654-61

Query Match 100.0%; Score 1761; DB 10; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGDSGNLTFTKVTYIEGVATISCOVNSKSDSVIQLNPNQOTYFRERPLKDSRFQ 60
DB 37 ITPGDGONLTFTKVTYIEGVATISCOVNSKSDSVIQLNPNQOTYFRERPLKDSRFQ 96
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; Sequence 61, Application US/09943851A
; Patent No. US20020150976A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher

;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kijavlin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tomas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/943, 851A
;; CURRENT FILING DATE: 2001-08-30
;; PRIOR APPLICATION NUMBER: US/09/866, 028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067, 411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069, 334
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;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020150976a1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020150976a1ember 30, 1999
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;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565

1 PRIOR FILING DATE: February 11, 2000
2 PRIOR APPLICATION NUMBER: PCT/US00/04414
3 PRIOR FILING DATE: February 22, 2000
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6 PRIOR APPLICATION NUMBER: PCT/US00/08439
7 PRIOR FILING DATE: March 30, 2000
8 PRIOR APPLICATION NUMBER: PCT/US00/14042
9 PRIOR FILING DATE: May 22, 2000
10 PRIOR APPLICATION NUMBER: PCT/US00/20710
11 PRIOR FILING DATE: July 28, 2000
12 PRIOR APPLICATION NUMBER: PCT/US00/32678
13 PRIOR FILING DATE: December 1, 2000
14 PRIOR APPLICATION NUMBER: PCT/US01/06520
15 PRIOR FILING DATE: February 28, 2001
16 NUMBER OF SEQ ID NOS: 120
17 SEQ ID NO 61
18 LENGTH: 440
19 TYPE: PRT
20 ORGANISM: Homo Sapien
21 US-09-943-851A-61

Query Match 100.0% Score 1761; DB 10; Length 440;
Best Local Similarity 100.0% Pred. No. 1.7e-105;
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Job time : 56 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 ; Search time 62.5 Seconds
(without alignments)
716.355 Million cell updates/sec

Title: US-09-778-187b-2_COPY_39_374

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1761	100.0	440	20	AAV17830
3	1761	100.0	440	21	AA23691
4	1761	100.0	440	22	AA23691
5	1761	100.0	442	21	AA23691
6	1761	100.0	442	21	AAV94341
7	1761	100.0	442	21	AAV94341
8	1761	100.0	442	23	AAE15887
9	1741	98.9	423	21	AAV45093
10	1704	96.8	364	21	AA25586

11	1612.5	91.6	443	22	AA23691
12	1591	90.3	419	21	AA23691
13	1134.5	64.4	229	21	AA23691
14	629	35.7	387	22	AA23691
15	623.5	35.4	444	20	AA23691
16	623.5	35.4	444	22	AA23691
17	604	34.3	388	22	AA23691
18	597	33.9	388	22	AA23691
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22	482.5	27.4	404	22	AA23691
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KW	diagnostics: forensic test; gene mapping; genetic disorder;	
KW	biotechnology; gene therapy; nutrition.	
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XX	WO200154477-A2.	
PN	02-AUG-2001.	
PD	25-JAN-2001: 2001WO-0502687.	
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PR	17-JUL-2000: 2000US-0617746.	
PR	03-AUG-2000: 2000US-0631451.	
PR	15-SEP-2000: 2000US-0663870.	
XX	(HYSE-) HYSEQ INC.	
PA	Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;	
PI	Cao Y, Drmanac RA, Zhang J, Weirman T;	
XX		

DR WPI; 2001-476164/51.
 DR N-PSDB; AAB98350.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX Claim 20; Page 877-878; 1275pp; English.
 PS
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 CC
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 1761; DB 22; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.8e-122;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 39 IPIGDSGNLFTKQVTVIEGEVATISCOVNSSDSVIQLNPNRQTIYFRDPRPLKDSRFQ 98
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 DB 99 LNFSSSELKVSLLNWSISDEGRYFCOLYNDPPQESTYTTITVLVPPRNLMIDIOKDTAVE 158
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 DT 12-AUG-1999 (first entry)
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 XX
 KW Human: PRO protein; tumour necrosis factor family; TNF; cytokine;
 KM secreted protein; transmembrane protein; inflammation disorder.
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 XX
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 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US25108.
 XX
 PR 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.

PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069694.
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 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 PA (GETH) GENENTECH INC.
 PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 PI Yuan J;
 XX
 XX WPI; 1999-371118/31.
 DR N-PSDB; AAX80055.
 XX
 PT Nucleic acids encoding PRO secreted and transmembrane proteins
 PS Claim 12; Fig 27; 123pp; English.
 CC
 CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 CC
 SQ Sequence 440 AA;
 Query Match 100.0%; Score 1761; DB 20; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-122;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IPIGDSGNLFTKQVTVIEGEVATISCOVNSSDSVIQLNPNRQTIYFRDPRPLKDSRFQ 60
 DB 37 IPIGDSGNLFTKQVTVIEGEVATISCOVNSSDSVIQLNPNRQTIYFRDPRPLKDSRFQ 96
 QY 61 LNFSSSELKVSLLNWSISDEGRYFCOLYNDPPQESTYTTITVLVPPRNLMIDIOKDTAVE 120
 DB 97 LNFSSSELKVSLLNWSISDEGRYFCOLYNDPPQESTYTTITVLVPPRNLMIDIOKDTAVE 156
 QY 121 GEEIEVNCCTAMASKPATTTIMFKGNTLKGSEVEEMSDMYTYSQMLKVHKEDGVPV 180
 DB 157 GEEIEVNCCTAMASKPATTTIMFKGNTLKGSEVEEMSDMYTYSQMLKVHKEDGVPV 216
 QY 181 ICQVEHPAVTGNLQOTORYLEVQYKRPQVHIQMTYPLQGLTREGALLETCEAIKGPQVMV 240
 DB 217 ICQVEHPAVTGNLQOTORYLEVQYKRPQVHIQMTYPLQGLTREGALLETCEAIKGPQVMV 276
 QY 241 TWWRVDEMPQHAHLVSGPNLFINNLTNDGTYRCEASNIYGAHSDMYLVYVDPPTTIP 300
 DB 277 TWWRVDEMPQHAHLVSGPNLFINNLTNDGTYRCEASNIYGAHSDMYLVYVDPPTTIP 336
 QY 301 PPTTTTTTTTTTTTTTTTTITDSRAGEEGSIRAVDH 336
 DB 337 PPTTTTTTTTTTTTTTTTTITDSRAGEEGSIRAVDH 372
 RESULT 3
 AAB01321
 ID AAB01321 standard; Protein; 440 AA.
 XX
 AC AAB01321;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Human PRO355 polypeptide.

XX	PRO: membrane bound protein; secreted protein; PRO327;
KW	PRO241; PRO115; PRO123; PRO299; PRO333; PRO344; PRO347;
KW	PRO353; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW	antibody; screening; detection; inhibition; probe; primer; human.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Peptide
FT	1..36
FT	/label= Signal peptide
FT	9..15
FT	/note= "N-myristoylation site"
FT	65..69
FT	/note= "N-glycosylation site"
FT	99..103
FT	/note= "N-glycosylation site"
FT	111..115
FT	/note= "N-glycosylation site"
FT	163..167
FT	/note= "N-glycosylation site"
FT	227..233
FT	/note= "N-myristoylation site"
FT	233..240
FT	/note= "Tyrosine kinase phosphorylation site"
FT	302..306
FT	/note= "N-glycosylation site"
FT	306..310
FT	/note= "N-glycosylation site"
FT	307..313
FT	/note= "N-myristoylation site"
FT	319..328
FT	/note= "Tyrosine kinase phosphorylation site"
FT	365..371
FT	/note= "N-myristoylation site"
FT	372..393
FT	/label= Transmembrane domain
FT	376..382
FT	/note= "N-myristoylation site"
FT	402..408
FT	/note= "N-myristoylation site"
FT	411..417
FT	/note= "N-myristoylation site"
FT	427..433
FT	/note= "N-myristoylation site"
FT	428..432
FT	/note= "N-myristoylation site"
FT	430..434
FT	/note= "N-glycosylation site"
XX	
PN	MO200032776-A2.
XX	
PD	08-JUN-2000.
XX	
PE	01-DEC-1999; 99MO-US28301.
XX	
PR	01-DEC-1998; 98MO-US25108.
PR	16-DEC-1998; 98US-0112850.
PR	22-DEC-1998; 98US-0113296.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Baker KP, Botstein D, Eaton DL, Ferrara N, Flivartoff E;
PI	Gertlisen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI	Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WJ;
XX	
DR	WPI: 2000-412324/35.
XX	
DR	N-PSDB: AAA49563.
XX	
PT	New human nucleic acids encoding secreted and transmembrane
PT	polypeptides, designated as PRO polypeptides, useful as pharmaceutical
XX	and diagnostic agents
XX	

PS	Claim 12;Fig 24; 187pp; English.
XX	
CC	New human nucleic acids encoding secreted and transmembrane
CC	polypeptides which are designated as PRO polypeptides are described
CC	The membrane-bound proteins have various industrial applications,
CC	including as pharmaceutical and diagnostic agents. The membrane-bound
CC	proteins can also be employed for screening of potential peptide or
CC	small molecule inhibitors of the relevant receptor/ligand interaction.
CC	Anti-PRO antibodies are useful for the affinity purification of PRO
CC	f rom recombinant cell culture or natural sources.
SQ	Sequence 440 AA;
XX	
XX	
Query Match	100.0%; Score 1761; DB 21; Length 440;
Best Local Similarity	100.0%; Pred. No. 2,1e-122;
Matches 336; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 IPTDGGNLFETKDVTVIEGEVATISCOVNKSDDSVIQLNPNRGTYFRDFRPLKDSRFQ 60
Dd	37 IPTDGGNLFTKDVTVEIEGEVATISCQVKNSSDSVIQLNPNRGTIFYFRDFRLKDSRFQ 96
OY	61 LFNSSSELKVLSTLNTNISDEGRFCOLYTDPQESYTTITVLVPNNLMIDIOGDVAE 120
Dd	97 LFNSSSELKVLSTLNVISDEGRFCOLYTDPEQESYTTITVLVPNNLMIDIOGDVAE 156
OY	121 GEELEVNSTAMASKPATTIMPFKGNTLELGKSEVEEMSMYTVTSQLMLKVHKEDDGVPV 180
Dd	157 GEELEVNSTAMASKPATTIMPFKGNTLELGKSEVEEMSDMYTTSQMLKVHKEBDGVPV 216
OY	181 ICQVENPAVTGNLTORYLEVOYKKPOVNIOMPTYPLGLTLREGDALETCEAIGKPQPVN 240
Dd	217 ICQVENPAVTGNLTORYLEVOYKKPOVNIOMPTYPLGLTLREDDALETCEAIGKQPQVV 276
OY	241 TWAVVDDEMPOHAFLSGPNLFINNNKKTNGTYRCBASNVGKAHSDPWLYYDDPRTIP 300
Dd	277 TWAVRDDEMPQHAAVLSGPNFLINNNKKTNDGTYRCBAASIVGKAHSIDPWLYYDDPRTIP 336
OY	301 PRTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH 336
Dd	337 PRTTTTTTTTTTTTTILTIITDSRAGEGSIRAVDH 372
Db	
RESULT 4	
AU029040	
ID	AU029040 standard; Protein; 440 AA.
XX	
AC	AU029040;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human PRO polypeptide sequence #17.
XX	
KW	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
RW	dogg; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KM	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX	
OS	Homo sapiens.
XX	
PX	M0200168848-A2.
PD	
XX	
PD	20-SEP-2001.
XX	
PF	28-FEB-2001; 2001MO-US06520.
XX	
PR	01-MAR-2000; 2000MO-US05601.
PR	02-MAR-2000; 2000MO-US05841.
PR	03-MAR-2000; 2000OUS-187202P.
PR	06-MAR-2000; 2000US-186968P.
PR	14-MAR-2000; 2000US-189328P.
PR	14-MAR-2000; 2000US-189328P.
PR	15-MAR-2000; 2000MO-US06884.
PR	21-MAR-2000; 2000OUS-190828P.

PR 21-MAR-2000; 2000US-191007P.
 PR 21-MAR-2000; 2000US-191048P.
 PR 21-MAR-2000; 2000US-191314P.
 PR 28-MAR-2000; 2000US-192655P.
 PR 29-MAR-2000; 2000US-193032P.
 PR 29-MAR-2000; 2000US-193053P.
 PR 30-MAR-2000; 2000OWO-US08439.
 PR 04-APR-2000; 2000US-194449P.
 PR 04-APR-2000; 2000US-194647P.
 PR 11-APR-2000; 2000US-195975P.
 PR 11-APR-2000; 2000US-196000P.
 PR 11-APR-2000; 2000US-196187P.
 PR 11-APR-2000; 2000US-196590P.
 PR 11-APR-2000; 2000US-196820P.
 PR 18-APR-2000; 2000US-198121P.
 PR 18-APR-2000; 2000US-198585P.
 PR 25-APR-2000; 2000US-199397P.
 PR 25-APR-2000; 2000US-199550P.
 PR 25-APR-2000; 2000US-199654P.
 PR 03-MAY-2000; 2000US-201516P.
 PR 17-MAY-2000; 2000OWO-US13705.
 PR 22-MAY-2000; 2000OWO-US14042.
 PR 30-MAY-2000; 2000OWO-US14941.
 PR 02-JUN-2000; 2000OWO-US15264.
 PR 05-JUN-2000; 2000US-209832P.
 PR 28-JUL-2000; 2000OWO-US20710.
 PR 22-AUG-2000; 2000US-0644848.
 PR 24-AUG-2000; 2000OWO-US23328.
 PR 08-NOV-2000; 2000OWO-US30952.
 PR 01-DEC-2000; 2000OWO-US32678.
 PR 20-DEC-2000; 2000OWO-US34956.
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;
 DR WPI; 2001-602746/68.
 XX N-PSDB; AAS45941.
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumours, such as prostate and breast tumours, in mammals and
 PT to screen for modulators of the compounds -
 PS
 XX Claim 11; Fig 34; 774pp; English.
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders.
 XX
 SQ Sequence 440 AA;

Query Match 100.0%; Score 1761; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-122;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPGDDGONLETKDYVTEGVATISCOVNSKSDSVIQLNPNRQTIYFRFRPLKDSRFQ 60
 DB 37 IPGDDGONLETKDYVTEGVATISCOVNSKSDSVIQLNPNRQTIYFRFRPLKDSRFQ 96

QY 61 LNFSSSELKVSILTNVISDEGRYFCOLYDTPDPOESYTTTIVLPPNNLMIDIOKDTAVE 120
 DB 97 LNFSSSELKVSILTNVISDEGRYFCOLYDTPDPOESYTTTIVLPPNNLMIDIOKDTAVE 156
 QY 121 GEEIEVNCITAMASKPATITIRFKGNTELKGSVEEWSDMATVTYSQMLKVKHKDDGVPV 180
 DB 157 GEEIEVNCITAMASKPATITIRFKGNTELKGSVEEWSDMATVTYSQMLKVKHKDDGVPV 216
 QY 181 ICQVEHPAVGNLQTOYRYLEVOYKPOVHIQMTYPLQSLTREGDALLETCEAIKGPQPVW 240
 DB 217 ICQVEHPAVGNLQTOYRYLEVOYKPOVHIQMTYPLQSLTREGDALLETCEAIKGPQPVW 276
 QY 241 TTVWRVDEMPQHAVLSCPNLFNNLNKTDNGYRCEASNTVGRKASHDYMUYVDPPTTIP 300
 DB 277 TTVWRVDEMPQHAVLSCPNLFNNLNKTDNGYRCEASNTVGRKASHDYMUYVDPPTTIP 336
 QY 301 PPTTTTTTTTTTTTTTTTTTTTDSRAGEGSTRAYDH 336
 DB 337 PPTTTTTTTTTTTTTTTTTTTTDSRAGEGSTRAYDH 372

RESULT 5

AA25619
 ID AAB25619 standard; Protein; 442 AA.
 XX
 AC AAB25619;
 XX
 DT 21-NOV-2000 (first entry)
 DE
 XX Protein encoded by human secreted protein gene #11.
 XX
 KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
 KW anticancer; vulnerrary; antiviral; antibacterial; antifungal;
 KW Immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200029435-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 27-OCT-1999; 99WO-US25031.
 XX
 PR 28-OCT-1998; 98US-0105971.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI NI J, Ruben SM, Olsen HS, Young PE, Kenny JT, Moore PA, Wei Y;
 PI Greene JM;
 XX WPI; 2000-387742/33.
 DR
 XX
 PT Isolated nucleic acid molecules encoding human secreted proteins are
 PT used for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases -
 PS
 XX Disclosure; Page 182-183; 803pp; English.
 CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given
 CC in AAB80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant;
 CC anti-inflammatory; antirheumatic; antirheumatic; dermatological;
 CC antiproliferative; antiarteriosclerotic; anticancer; vulnerrary;
 CC antiviral; antibacterial; and antifungal activity. The proteins,

CC polypeptides, agonists and antagonists may be used to treat prevent
 CC and/or diagnose various disease, disorders and conditions examples of
 CC which include: immune disorders e.g. Addison's disease, rheumatoid
 CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
 CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
 CC hyperproliferative disorders such as paraproctenomas and purpura;
 CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
 CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
 CC sequences may also be used in wound healing and the treatment of
 CC infectious diseases. The human secreted protein gene #11 and protein
 CC sequences are represented in sequences AAA80616 and AAB25586. Sequences
 CC AAA80677-A80682 represent genes related to the secreted protein gene#11.
 XX
 SQ Sequence 442 AA:
 Query Match 100.0%; Score 1761; DB 21: Length 442;
 Best Local Similarity 100.0%; Pred. No. 2, Le-122;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IPTGDCQLFTKDVIVIEGEVATISCVNKSDDSVIQLNPNRQTYFRDPRPKDSRFQ 60
 DB 39 IPTGDCQLFTKDVIVIEGEVATISCVNKSDDSVIQLNPNRQTYFRDPRPKDSRFQ 98
 QY 61 LNFSSSELKVSITNNSIDEGRYFCQLYTDPPQESYTTITVLPNNLMIDIQKTAVE 120
 DB 99 LNFSSSELKVSITNNSIDEGRYFCQLYTDPPQESYTTITVLPNNLMIDIQKTAVE 158
 QY 121 GEIEVNCAMASKPATTTIRMFKNTELKGSSEVEMSDMYTTSOLMLKVKHEDGVPY 180
 DB 159 GEIEVNCAMASKPATTTIRMFKNTELKGSSEVEMSDMYTTSOLMLKVKHEDGVPY 218
 QY 181 ICQVHPAVTGNLQTOYRLEVQYKQVNIQMTYPLQGLTREGDALELTCEAIGKQPVMY 240
 DB 219 ICQVHPAVTGNLQTOYRLEVQYKQVNIQMTYPLQGLTREGDALELTCEAIGKQPVMY 278
 QY 241 TWVRVDEMPQVNAVLSGPNLFINLNKTDNGYRCEASNYGKAHSDYMLYVDPPTTIP 300
 DB 279 TWVRVDEMPQVNAVLSGPNLFINLNKTDNGYRCEASNYGKAHSDYMLYVDPPTTIP 338
 QY 301 PPTTTTTTTTTTTTTTTTTTTSDRAGEGSIKRAVDH 336
 DB 339 PPTTTTTTTTTTTTTTTTTTTSDRAGEGSIKRAVDH 374
 RESULT 6
 AAY94341
 ID AAY94341 standard; Protein; 442 AA.
 XX
 AC AAY94341:
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human cell surface receptor protein #8.
 XX
 KW Human; HCSRNP; cytoskeletal; antiarthritic; antirheumatic; antistimatic;
 KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
 KW neuroprotective; nocrotropic; anticonvulsant; cancer; leukaemia;
 KW melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia;
 KW Alzheimer's diseases; multiple sclerosis; epilepsy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..44
 FT Protein /label= Signal_peptide
 FT Protein 45..442
 FT Protein /label= HCSRNP-8
 FT Protein 57..126
 FT Protein /label= Immunoglobulin_domain
 FT Protein 159..222
 FT Protein /label= Immunoglobulin_domain
 FT Protein 260..315
 FT Protein /label= Immunoglobulin_domain

FT Domain 375..394
 FT /label= Transmembrane_domain
 FT Region 53
 FT /note= "potential phosphorylation site"
 FT Region 67
 FT /note= "potential glycosylation site"
 FT Region 101
 FT /note= "potential glycosylation site"
 FT Region 103
 FT /note= "potential phosphorylation site"
 FT Region 113
 FT /note= "potential glycosylation site"
 FT Region 115
 FT /note= "potential phosphorylation site"
 FT Region 155
 FT /note= "potential phosphorylation site"
 FT Region 165
 FT /note= "potential glycosylation site"
 FT Region 176
 FT /note= "potential phosphorylation site"
 FT Region 190
 FT /note= "potential phosphorylation site"
 FT Region 233
 FT /note= "potential phosphorylation site"
 FT Region 241
 FT /note= "potential phosphorylation site"
 FT Region 304
 FT /note= "potential glycosylation site"
 FT Region 308
 FT /note= "potential glycosylation site"
 FT Region 310
 FT /note= "potential phosphorylation site"
 FT Region 329
 FT /note= "potential phosphorylation site"
 FT Region 368
 FT /note= "potential phosphorylation site"
 FT Region 432
 FT /note= "potential glycosylation site"
 XX
 XX MO200028032-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 12-NOV-1999; 99WO-US26742.
 XX
 PR 12-NOV-1998; 98US-0191280.
 PR 07-DEC-1998; 98US-0206647.
 PR 08-MAR-1999; 99US-0123404.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
 PI Hillman JL, Bandman O, Azimzal Y, Au-Young J;
 XX
 DR WPI: 2000-376546/32.
 DR N-PSDB: AAA27051.
 XX
 PT New human cell surface receptor protein and polynucleotide useful for
 PT diagnosis, prevention and treatment of cancer, immune disorders,
 PT infection and neuronal disorders -
 XX
 PS Claim 1: Page 81-82; 97pp; English.
 XX
 CC The present sequence is a novel human cell surface receptor protein
 CC (HCSRNP) designated HCSRNP-8. The nucleotide sequence was identified in
 CC Incyte Clone 312256 from the cDNA library LUNGNOT02, which was made from
 CC RNA isolated from lung tissue. A number of Incyte clones were used to
 CC assemble the consensus sequence. BLAST analysis showed that the sequence
 CC is homologous to immunosuppressant protein B12 g3779242. HCSRNP and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSRNP. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,

CC bacterial and parasitic infections and neuronal disorders such as
 CC akathesia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HSCRPs may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibody may be used as
 CC antagonists, as a targeting or delivery mechanism for binding
 CC pharmaceutical agents into contact with cells or tissues expressing
 CC HCSR and for diagnosis of HCSR-related disorders. HCSR and its
 CC catalytic or immunogenic fragments are useful for drug screening using
 CC libraries of compounds.

XX Sequence 442 AA;

Query Match 100.0%; Score 1761; DB 21; Length 442;
 Best Local Similarity 100.0%; Pred. No. 2.1e-122;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGDSGNLFTKDVYIEGEVATISCOVNSDSDSVIQLNPNRQTIYFRDRPLKDSRFQ 60
 DB 39 IPTGDSGNLFTKDVYIEGEVATISCOVNSDSDSVIQLNPNRQTIYFRDRPLKDSRFQ 98
 QY 61 LNFSSSELKVSILTNVISDEGRYFCOLYTDPPQESYTTIVLVPPRNLMDIDOKTAVE 120
 DB 99 LNFSSSELKVSILTNVISDEGRYFCOLYTDPPQESYTTIVLVPPRNLMDIDOKTAVE 158
 QY 121 GEEIEVNCSTAMASKPATITRMFKGNTELKSGSEVEMSDMTYTSQMLKVKHKEDGVPV 180
 DB 159 GEEIEVNCSTAMASKPATITRMFKGNTELKSGSEVEMSDMTYTSQMLKVKHKEDGVPV 218
 QY 181 ICQVEHNAVGNLQOTQRYLEVQYKRPVNIOMTYPLQGLTREGDALELTCEAIKGPQVPMV 240
 DB 219 ICQVEHNAVGNLQOTQRYLEVQYKRPVNIOMTYPLQGLTREGDALELTCEAIKGPQVPMV 278
 QY 241 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGAHSDYMLVYVDPPTIP 300
 DB 279 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGAHSDYMLVYVDPPTIP 338
 QY 301 PPTTTTTTTTTTTTTITITTSRAGEGSTRAYDH 336
 DB 339 PPTTTTTTTTTTTTTITITTSRAGEGSTRAYDH 374

RESULT 7

AA45092 ID AA45092 standard; Protein: 442 AA.

XX AA45092;

XX 31-MAY-2000 (first entry)

DE Human lymphoid derived dendritic cell adhesion molecule.

XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
 KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
 KW biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..374 /label= Extracellular_domain

FT Peptide 1..38 /label= Leader_peptide

FT Protein 39..442 /label= Mature_human_LDCAM_polypeptide

FT Modified-site 67..69 /note= "N-Glycosylation site"

FT Modified-site 101..103 /note= "N-Glycosylation site"

FT Modified-site 113..115 /note= "N-Glycosylation site"

FT Modified-site 165..167 /note= "N-Glycosylation site"

FT /note= "N-Glycosylation site"
 FT 304..306
 FT /note= "N-Glycosylation site"
 FT 308..310
 FT Modified-site
 FT 375..395
 FT /note= "N-Glycosylation site"
 FT 375..395
 FT /label= Transmembrane_domain
 FT 396..442
 FT /label= Cytoplasmic_domain

XX W0200008158-A2.

XX 17-FEB-2000.

XX 05-AUG-1999; 99WC-U517905.

XX 07-AUG-1998; 98US-0095672.

XX (IMMUNEX CORP.

XX Baum PR, Fanslow WC;

XX WPI; 2000-205712/18.

XX N-PSDB: AAZ50882.

XX Novel molecules designated LDCAM are capable of altering or modulating
 T cell function

XX Claim 7; Page 42-43; 44pp; English.

XX The present amino acid sequence is the human lymphoid derived dendritic
 CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
 CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
 CC region of B7-1. Human LDCAM is expressed in breast, retina, foetal
 CC liver, spleen and heart, lung, muscle, placenta, thyroid and lung
 CC carcinoma. LDCAM polypeptides interact with T cell surface molecules
 CC to alter signalling and inhibits T cell proliferation, bind to
 CC themselves and B7L-1, an LDCAM binding protein and increases natural
 CC killer (NK) cell populations. It may be used to measure the biological
 CC activity and as quality control reagents of LDCAM binding proteins.
 CC LDCAM may be used for treating disorders associated with malfunctioning
 CC of immune system, inflammation, autoimmune disorders, viral infected
 CC cells, infectious diseases and for killing tumour cells. They are also
 CC useful for prevention or reducing the effect of organ and bone marrow
 CC transplant rejection and for modulating T cell immune responses. LDCAM
 CC polypeptides may also be used as carriers for delivering agents attached
 CC to T cells or cells bearing B7L-1.

XX Sequence 442 AA;

Query Match 100.0%; Score 1761; DB 21; Length 442;

Best Local Similarity 100.0%; Pred. No. 2.1e-122;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGDSGNLFTKDVYIEGEVATISCOVNSDSDSVIQLNPNRQTIYFRDRPLKDSRFQ 60
 DB 39 IPTGDSGNLFTKDVYIEGEVATISCOVNSDSDSVIQLNPNRQTIYFRDRPLKDSRFQ 98
 QY 61 LNFSSSELKVSILTNVISDEGRYFCOLYTDPPQESYTTIVLVPPRNLMDIDOKTAVE 120
 DB 99 LNFSSSELKVSILTNVISDEGRYFCOLYTDPPQESYTTIVLVPPRNLMDIDOKTAVE 158
 QY 121 GEEIEVNCSTAMASKPATITRMFKGNTELKSGSEVEMSDMTYTSQMLKVKHKEDGVPV 180
 DB 159 GEEIEVNCSTAMASKPATITRMFKGNTELKSGSEVEMSDMTYTSQMLKVKHKEDGVPV 218
 QY 181 ICQVEHNAVGNLQOTQRYLEVQYKRPVNIOMTYPLQGLTREGDALELTCEAIKGPQVPMV 240
 DB 219 ICQVEHNAVGNLQOTQRYLEVQYKRPVNIOMTYPLQGLTREGDALELTCEAIKGPQVPMV 278
 QY 241 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGAHSDYMLVYVDPPTIP 300
 DB 279 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGAHSDYMLVYVDPPTIP 338

PS Claim 7; Page 46-47; 44pp; English.

XX The present amino acid sequence is the mouse lymphoid derived dendritic

CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic

CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic

CC region of B7-L1. Mouse LDCAM is found on whole embryo, testes, triple

CC negative cells murine splenic and lymph node CD8+, 549.1 and dendritic

CC cells. LDCAM polypeptides interact with T cell surface molecules

CC to alter signalling and inhibits T cell proliferation, bind to

CC themselves and B7L-1, an LDCAM binding protein and increases natural

CC killer (NK) cell populations. It may be used to measure the biological

CC activity and as quality control reagents of LDCAM binding proteins.

CC LDCAM may be used for treating disorders associated with malfunctioning

CC of immune system, inflammation, autoimmune disorders, viral infected

CC cells, infectious diseases and for killing tumour cells. They are also

CC useful for prevention or reducing the effect of organ and bone marrow

CC transplant rejection and for modulating T cell immune responses. LDCAM

CC polypeptides may also be used as carriers for delivering agents attached

CC to T cells or cells bearing B7L-1.

XX

XX Sequence 423 AA:

SQ

Query Match 98.9%; Score 1741; DB 21; Length 423;

Best Local Similarity 98.8%; Pred. No. 5.9e-121;

Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDSGNLFTKDVTEIEGEVATISCOVNSSDSVIQLNPNRQTYFRDPRPLKDSRFQ 60

DB 21 IPTGDSGNLFTKDVTEIEGEVATISCOVNSSDSVIQLNPNRQTYFRDPRPLKDSRFQ 80

QY 61 LNFSSSELKVSILTNVISISDEGRFCOLYTDPPQESTTTITVLVPRNLMIDIOKTAVE 120

DB 81 LNFSSSELKVSILTNVISISDEGRFCOLYTDPPQESTTTITVLVPRNLMIDIOKTAVE 140

QY 121 GEEIEVNCSTAMASKPATITTFMFKGNTLKGKSEYEEMSDMYTYSQMLKVHKEDGVPV 180

DB 141 GEEIEVNCSTAMASKPATITTFMFKGNTLKGKSEYEEMSDMYTYSQMLKVHKEDGVPV 200

QY 181 ICQVEHNAVGNLQTORRYLEVOYKRPQVHIQMTYRPLQGLTREGDALETCEAIKRPQVMV 240

DB 201 ICQVEHNAVGNLQTORRYLEVOYKRPQVHIQMTYRPLQGLTREGDALETCEAIKRPQVMV 260

QY 241 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNTVGRASHDYMLYVDPPTTIP 300

DB 261 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNTVGRASHDYMLYVDPPTTIP 320

QY 301 PPTTTTITTTTTTTTTITITDSRAGEGSIKRAVDH 336

DB 321 PPTTTTITTTTTTTTTITITDSRAGEGSIKRAVDH 356

RESULT 10

AAB25586

ID AAB25586 standard; protein; 364 AA.

XX

XX AAB25586;

XX

XX 21-NOV-2000 (first entry)

XX

DE Protein encoded by human secreted protein gene #11.

XX

KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;

KW antihemmatic; dermatological; antiproliferative; antiarteriosclerotic;

KW anticancer; vulnary; antiviral; antibacterial; antifungal;

KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;

KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;

KW Crohn's disease; nephritis; hyperproliferative disorder;

KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;

KW melanoma; lymphoma; wound healing; human.

XX

OS Homo sapiens.

XX

PN WO200029435-A1.

XX

PD 25-MAY-2000.

XX

XX 27-OCT-1999; 99WO-US25031.

PF

XX

XX 28-OCT-1998; 98US-0105971.

PR

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI N1 J. Ruben SM, Olsen HS, Young PE, Kenny JT, Moore PA, Wei Y;

PI Greene JM;

XX

XX WPI; 2000-387742/33.

DR

XX

XX N-PDSB; AAA80616.

PT

PT Isolated nucleic acid molecules encoding human secreted proteins are

PT used for the prevention, amelioration and treatment of autoimmune,

PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,

PT wounds, and infectious diseases -

XX

PS Claim 1; Figure 28A-B; 803pp; English.

XX

CC The present invention relates to 12 secreted human proteins and the

CC nucleotide sequences encoding them. The polynucleotide sequences given

CC in AAA80606-A80623 encode the 12 secreted protein sequences given in

CC AAB25576-B25593. The human secreted proteins have various activities

CC dependent on the tissues in which they are expressed. Examples of the

CC activities of the proteins include: immunosuppressant;

CC anti-inflammatory; antiarthritic; antirheumatic; dermatological;

CC antiproliferative; antiarteriosclerotic; anticancer; vulnary;

CC antiviral; antibacterial; and antifungal activity. The proteins,

CC polypeptides, agonists and antagonists may be used to treat prevent

CC and/or diagnose various disease, disorders and conditions examples of

CC which include: immune disorders e.g. Addison's disease, rheumatoid

CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders

CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;

CC hyperproliferative disorders such as paraprothemia and purpura;

CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;

CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide

CC sequences may also be used in wound healing and the treatment of

CC infectious diseases. The human secreted protein gene #11 and protein

CC sequences are represented in sequences AAA80616 and AAB25586. Sequences

CC AAA80677-A80682 represent genes related to the secreted protein gene#11.

XX

SQ

Sequence 364 AA:

Query Match 96.8%; Score 1704; DB 21; Length 364;

Best Local Similarity 100.0%; Pred. No. 2.7e-118;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGDSGNLFTKDVTEIEGEVATISCOVNSSDSVIQLNPNRQTYFRDPRPLKDSRFQ 60

DB 39 IPTGDSGNLFTKDVTEIEGEVATISCOVNSSDSVIQLNPNRQTYFRDPRPLKDSRFQ 98

QY 61 LNFSSSELKVSILTNVISISDEGRFCOLYTDPPQESTTTITVLVPRNLMIDIOKTAVE 120

DB 99 LNFSSSELKVSILTNVISISDEGRFCOLYTDPPQESTTTITVLVPRNLMIDIOKTAVE 158

QY 121 GEEIEVNCSTAMASKPATITTFMFKGNTLKGKSEYEEMSDMYTYSQMLKVHKEDGVPV 180

DB 159 GEEIEVNCSTAMASKPATITTFMFKGNTLKGKSEYEEMSDMYTYSQMLKVHKEDGVPV 218

QY 181 ICQVEHNAVGNLQTORRYLEVOYKRPQVHIQMTYRPLQGLTREGDALETCEAIKRPQVMV 240

DB 219 ICQVEHNAVGNLQTORRYLEVOYKRPQVHIQMTYRPLQGLTREGDALETCEAIKRPQVMV 278

QY 241 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNTVGRASHDYMLYVDPPTTIP 300

DB 279 TWRVVDDEMPQHAVLSGPNLFINNLTNDGTGRCEASNTVGRASHDYMLYVDPPTTIP 338

QY 301 PPTTTTITTTTTTTTTITITDSRA 325

DB 339 PPTTTTITTTTTTTTTITITDSRA 363

RESULT 11
 AAB88427
 ID AAB88427 standard; Protein: 443 AA.
 XX AAB88427;
 XX 23-MAY-2001 (first entry)
 DT
 DE Human membrane or secretory protein clone PSEC0200.
 XX
 KM Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes.
 XX
 OS Homo sapiens.
 XX
 PN EPI067182-A2.
 PD 10-JAN-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 DR WPI; 2001-093989/11.
 DR N-PSDB; AAF93854.
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX
 PS Claim 1: SEQ ID 222; 609pp + CD ROM; English.
 XX
 XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.
 CC
 SO Sequence 443 AA:
 Query Match 91.6%; Score 1612.5; DB 22: Length 443;
 Best Local Similarity 92.6%; Pred. No. 2.1e-111;
 Matches 312; Conservative 4; Mismatches 20; Indels 1; Gaps 1;
 OY 1 IPGDDONLFTKQVTVTEGEVATISCOVNSDSVIOQLPNQOTYFERPRPLKDSRFQ 60
 DB 39 IPTGDDONLFTKQVTVTEGEVATISCOVNSDSVIOQLPNQOTYFERPRPLKDSRFQ 98

OY 61 LNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTITVLVPPRNLMDIOKDTAVE 120
 DB 99 LNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTITVLVPPRNLMDIOKDTAVE 158
 OY 121 GEELEVNCSTAMASKPATTTIMFKGNTELKSKSEVEEMSDMTYTSQMLKVHKEDDGPV 180
 DB 159 GEELEVNCSTAMASKPATTTIMFKGNTELKSKSEVEEMSDMTYTSQMLKVHKEDDGPV 218
 OY 181 ICOVEHPAVTGNLOTORYLEVOYKPOVHIQMTYPLQGLTREGDALLETCEAIGKPOPVN 240
 DB 219 ICOVEHPAVTGNLOTORYLEVOYKPOVHIQMTYPLQGLTREGDALLETCEAIGKPOPVN 278
 OY 241 TWRVVDDEMPQHAVLSCPNLFINNLNKTDNGTYRCEASNIVGKNSDYMVYVDPPTTIP 300
 DB 279 TWRVVDDEMPQHAVLSCPNLFINNLNKTDNGTYRCEASNIVGKNSDYMVYVDTATTE 338
 OY 301 PPTTTTTTTTTTTTTT-LTITDSRAGEEGSIRAVDH 336
 DB 339 PAVHGLTQLPNSAEELDESDLSRAGEEGSIRAVDH 375
 RESULT 12
 AAY53028
 ID AAY53028 standard; Protein: 414 AA.
 XX
 AC AAY53028;
 XX
 DT 29-FEB-2000 (first entry)
 XX
 DE Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
 XX
 KM Human; secreted protein; nutritional; cytokine; cell proliferation;
 KM differentiation; immune stimulating; vaccine; suppression;
 KW haematopoiesis regulation; tissue growth; activin; inhibin;
 KW chemotactic; chemokine; haemostatic; thrombolytic; receptor;
 KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
 KW tumour inhibition; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09957132-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 07-MAY-1999; 99WC-US09970.
 XX
 PR 07-MAY-1998; 98US-0084564.
 PR 02-JUN-1998; 98US-0087645.
 PR 22-JUL-1998; 98US-0093712.
 PR 31-JUL-1998; 98US-0094935.
 PR 10-AUG-1998; 98US-0095880.
 PR 11-AUG-1998; 98US-0096068.
 PR 06-MAY-1999; 99US-0096068.
 XX
 PA (GENY) GENETICS INST INC.
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Tracy M, Agostino MJ, Steininger RJ, Bowman MR;
 PI DIBlasio-Smith E, Widom A;
 DR WPI; 2000-052937/04.
 DR N-PSDB; AA233346.
 XX
 PT New polynucleotides encoding secreted human proteins, derived from
 PT adult placenta, adult retina, fetal brain, fetal -
 XX
 PS Claim 71: Page 416-417; 492pp; English.
 XX
 CC The present invention describes new human secreted proteins which were
 CC isolated from adult placenta, adult retina, foetal brain, foetal kidney,
 CC adult blood, adult brain, adult thyroid, adult bladder, adult neural
 CC tissue, adult testes, and adult lymph node cDNA libraries. The human

CC secreted proteins, and the polynucleotides encoding them, are predicted
 CC to have biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals. Suggested activities include nutritional activity, cytokine
 CC and cell proliferation/differentiation activity, immune stimulating
 CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC catherin/tumour invasion suppressor activity, and tumour inhibition
 CC activity. The polynucleotides are also stated to be useful for gene
 CC therapy. AAB25593 to AAB25598 encode human secreted proteins, and
 CC AAB25998 to AAB25960 represent human secreted proteins, given in the
 CC present invention.

CC Sequence 414 AA;

Query Match 90.3%; Score 1591; DB 21; Length 414;
 Best Local Similarity 91.7%; Pred. No. 7.5e-110;
 Matches 308; Conservative 0; Mismatches 0; Indels 28; Gaps 1;

QY 1 IPTGDCNLEFTKDYVIEGEVATISCOVNSDDSVIOLLNPNROTIFYRDFRPLKDSRFQ 60
 DB 39 IPTGDCNLEFTKDYVIEGEVATISCOVNSDDSVIOLLNPNROTIFYRDFRPLKDSRFQ 98
 QY 61 LNFSSSELYSLTNVSISSDEGRYFCOLYDPPQESYTTITVLPVPRMLIDIKDAVE 120
 DB 99 LNFSSSELYSLTNVSISSDEGRYFCOLYDPPQESYTTITVLPVPRMLIDIKDAVE 158
 QY 121 GEEIEVNCNTAASKPATITRMFKGNTLKGSEVEMSDMTYVSQMLKYNKEDDGPV 180
 DB 159 GEEIEVNCNTAASKPATITRMFKGNTLKGSEVEMSDMTYVSQMLKYNKEDDGPV 218
 QY 181 ICQVEHNAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRREGDALELTCEAIGKRPQVMV 240
 DB 219 ICQVEHNAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRREGDALELTCEAIGKRPQVMV 278
 QY 241 TWVAVDEMPQHAVLGGPNLFINNLKNTDNGTYRCEASNIYKRAHSDMYLVDPPTTIP 300
 DB 279 TWVAVDEMPQHAVLGGPNLFINNLKNTDNGTYRCEASNIYKRAHSDMYLVY----- 331
 QY 301 PPTTTTTTTTTTTTTLITITDSRAGEGSTRADVH 336
 DB 332 -----DSRAGEGSTRADVH 346

RESULT 13
 AAB25593

ID AAB25593 standard; Protein; 229 AA.

AC AAB25593;

DT 21-NOV-2000 (first entry)

DE Protein encoded by human secreted protein gene #11 clone H00D81.

XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
 KW anticancer; vulnerrary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human.

XX Homo sapiens.

PN WO200029435-A1.

XX 25-MAY-2000.

PF 27-OCT-1999; 99WO-US25031.

PR 28-OCT-1998; 98US-0105971.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX NI J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
 PI Greene JM;
 DR WPI: 2000-387742/33.

PT Isolated nucleic acid molecules encoding human secreted proteins are
 PT used for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases.

PS Claim 1; Page 685-686; 803pp; English.

CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given
 CC in AAB80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant;
 CC anti-inflammatory; antiarthritic; antirheumatic; dermatological;
 CC antiproliferative; antiarteriosclerotic; anticancer; vulnerrary;
 CC antiviral; antibacterial; and antifungal activity. The proteins,
 CC polypeptides, agonists and antagonists may be used to treat prevent
 CC and/or diagnose various disease, disorders and conditions examples of
 CC which include: immune disorders e.g. Addison's disease, rheumatoid
 CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
 CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
 CC hyperproliferative disorders such as paraprothelhaemias and purpura;
 CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
 CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
 CC sequences may also be used in wound healing and the treatment of
 CC infectious diseases. The human secreted protein gene #11 and protein
 CC sequences are represented in sequences AAB80616 and AAB25586. Sequences
 CC AAB80677-A80682 represent genes related to the secreted protein gene#11.

XX Sequence 229 AA;

Query Match 64.4%; Score 1134.5; DB 21; Length 229;
 Best Local Similarity 96.0%; Pred. No. 2.4e-76;
 Matches 216; Conservative 2; Mismatches 0; Indels 7; Gaps 1;

QY 110 MIDIOKDTAVGEEIEVNCNTAASKPATITRMFKGNTLKGSEVEMSDMTYVSQML 169
 DB 1 MIDIOKDTAVGEEIEVNCNTAASKPATITRMFKGNTLKGSEVEMSDMTYVSQML 60
 QY 170 KVHKEDDGPVICOVEHNAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRREGDALELTG 229
 DB 61 KVHKEDDGPVICOVEHNAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRREGDALELTG 120
 QY 230 EATGKPPQVWVWVAVRVDDEMPQHAVLGGPNLFINNLKNTDNGTYRCEASNIYKRAHSDYM 289
 DB 121 EATGKPPQVWVWVAVRVDDEMPQHAVLGGPNLFINNLKNTDNGTYRCEASNIYKRAHSDYM 180
 QY 290 LVYVDPPTTIPPTTT 327
 DB 181 LVYVDPPTTIPPTTT 1:1
 1:1

RESULT 14

ID AAM78418 standard; Protein; 387 AA.

AC AAM78418;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1080.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;


```
QY 66 SSELKVSINVSISDEGRYFCQLYTDPPESEYTTITIVLPPRNLMIDIQKOTAVEGEIE 125
Db 93 WHELSISVSIVSLSDGQYCSLFTMPVKTSKAVLTVLGVPEKPOISGFSSPVMEGDIHQ 152
QY 126 VNCJAMASKRPATITRMFKGNTLKGKSEVEEMS---DMYTVTSQMLKVKHKEDDGVPIIC 182
Db 153 LTCKTSGSKPPAADIRMFKNKDKETKDVKYLKEEDANKRKTFTVSSTLDFRVDRSDDGVAVIC 212
QY 183 QVEHPAVTGNLQ--TORYLEVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOPMVT 241
Db 213 RVDHESINATPPQYAMQVLEIHYTPSVKI---IPSTPPQEGQPLILTCESKGKPLPEPVL 269
QY 242 WVRVDEM--POHAYLSGPNLFINNLKNTDNGTYRCEASNI VGRKASDYMLYYDPPPTT 299
Db 270 WTKDGGELPDPDRMVVSGRELNIILFNKKTNDNGTYRCEATNTIGSSAEYVLIYHVDVPNTL 329
QY 300 PPPTTTTTTTTTTTTTTTTTIT-----DSRAGEEGSIRAVDH 336
Db 330 LPTTIIIPSLTTATVTTVAITTSPTTSATTSIRDPNALAGONGP---DH 376
```

Search completed: November 20, 2002, 07:37:56
Job time : 65.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 ; Search time 28.5 Seconds
(without alignments)
2429,187 Million cell updates/sec

Title: US-09-778-187B-2_COPY_39_374

Perfect score: 1761
Sequence: 1 IPTGDSQNLFTKDVYIEGE.....LTIIDSRAGEGSRIVADH 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	99.8	442	4	Q9BY67
2	1741	98.9	445	11	Q8R4L1
3	1725.5	98.0	456	11	Q8R5M8
4	1725.5	98.0	494	11	Q9CRY3
5	1529	86.8	336	11	Q9D6E7
6	1180	67.0	295	11	Q9Z2H8
7	1157.5	65.7	306	11	Q9QYL4
8	1137	64.6	295	11	Q9QYL6
9	1048	59.5	289	11	Q9QYL5
10	1024.5	58.2	278	11	Q9QYL3
11	622	35.3	388	11	Q8R464
12	609	34.6	381	4	Q9Y4A4
13	482.5	27.4	396	11	Q99N28
14	469.5	26.7	432	4	Q9UJPI
15	301	17.1	549	11	Q9D006
16	298	16.9	549	11	Q9JLB9

17	292	16.6	549	4	Q9NQS3	Q9nq3 homo sapien
18	277.5	15.8	438	11	Q9JLB7	Q9jlb7 mus musculu
19	277.5	15.8	510	11	Q9JLB8	Q9jlb8 mus musculu
20	263.5	15.0	5198	5	Q76518	Q76518 caenorhabdi
21	250	14.2	439	13	Q57349	Q57349 gallus gall
22	248	14.1	407	4	Q9Y4I2	Q9y4i2 homo sapien
23	243	13.8	725	13	Q73633	Q73633 xenopus lae
24	243	13.8	1482	5	Q9V4Y0	Q9v4y0 drosophila
25	235	13.3	393	4	Q95727	Q95727 homo sapien
26	227	12.9	4162	13	Q98918	Q98918 gallus gall
27	224.5	12.7	605	4	Q96184	Q96184 homo sapien
28	223.5	12.7	7962	4	Q10465	Q10465 homo sapien
29	223.5	12.7	34350	4	Q8W422	Q8w422 homo sapien
30	223	12.7	725	13	Q73634	Q73634 xenopus lae
31	222	12.6	467	11	Q91VW9	Q91vw9 mus musculu
32	222	12.6	1380	4	Q9HCK2	Q9hck2 homo sapien
33	222	12.6	1675	13	Q98SM4	Q98sm4 brachydanto
34	221	12.5	344	11	Q99PJ0	Q99pj0 mus musculu
35	220	12.5	344	4	Q9E121	Q9e121 homo sapien
36	220	12.5	449	4	Q9UEI6	Q9uei6 homo sapien
37	219	12.4	344	13	Q9DF61	Q9df61 gallus gall
38	219	12.4	1060	11	Q9QZ13	Q9qz13 rattus norv
39	218	12.4	1032	13	Q8UVD6	Q8uvd6 brachydanto
40	217.5	12.4	959	5	Q9N9Y9	Q9n9y9 drosophila
41	217.5	12.4	968	5	Q9W4T9	Q9w4t9 drosophila
42	217	12.3	417	4	Q96BJ1	Q96bj1 homo sapien
43	216.5	12.3	975	5	Q97174	Q97174 drosophila
44	216.5	12.3	1270	5	Q9U3P2	Q9u3p2 caenorhabdi
45	216	12.3	392	11	Q92314	Q92314 mus musculu

ALIGNMENTS

RESULT 1

Q9BY67 PRELIMINARY; PRT; 442 AA.

AC Q9BY67; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Necdin-like protein 2.

GN NECN2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;

RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin superfamily".

RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF132811; AAF69029.1; -

DR InterPro: IPR003598; Ig.

DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR003600; Ig_Like.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_3.

DR SMART; SM00409; Ig_3.

DR SMART; SM00408; IGC2; 3.

DR SMART; SM00410; IG_Like; 2.

KW Immunoglobulin domain.

SO SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 99.8%; Score 1758; DB 4; Length 442;
Best Local Similarity 99.7%; Pred. No. 6,7e+139;
Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGDSQNLFTKDVYIEGEVATISCOVKNKSDSVTOLLNPNKQTYFRDPRFKDSRP 60
DB 39 IPTGDSQNLFTKDVYIEGEVATISCOVKNKSDSVTOLLNPNKQTYFRDPRFKDSRP 98

QY	61	LNLFSSSEKLKSLTNVSI	SDSGRCFCOLYD	PPDESTTITVLY	PPNNMIDIOKTPAE	120
Db	99	LNLFSSSEKLKSLTNVSI	SDSGRCFCOLYD	PPDESTTITVLY	PPNNMIDIOKTPAE	158
QY	121	GEEIEVNCSTAMASKPAT	TIKFKGNTELBKSE	VEEWSDMYTV	SOLMLKVHKEDDGVY	180
Db	159	GEEIEVNCSTAMASKPAT	TIKFKGNTELBKSE	VEEWSDMYTV	SOLMLKVHKEDDGVY	218
QY	181	ICQYEHNAVITNLOTORT	LEYQYKPYVHIOMTY	PLGLTREGSALFETCA	ICKPOPVWY	240
Db	219	ICQYEHNAVITNLOTORT	LEYQYKPYVHIOMTY	PLGLTREGSALFETCA	ICKPOPVWY	278
QY	241	TWVRVDEDMPOHAYL	SGPNLFINNLKNTD	NGTYRCEASNIVG	KAHSDYMLVYDDEPTIIP	300
Db	279	TWVRVDEDMPOHAYL	SGPNLFINNLKNTD	NGTYRCEASNIVG	KAHSDYMLVYDDEPTIIP	338
QY	301	PPTTTTTTTTTTTTTIT	ITITDSAGEGSI	RAVDH	336	
Db	339	PPTTTTTTTTTTTTTIT	ITITDSAGEGSI	RAVDH	374	

RESULT 2	08R4L1	PRELIMINARY:	PRT:	445 AA.
ID	08R4L1			
AC	08R4L1;			
DT	01-JUN-2002 (Tremblrel, 21, Created)			
DT	01-JUN-2002 (Tremblrel, 21, Last sequence update)			
DT	01-JUN-2002 (Tremblrel, 21, Last annotation update)			
DE	Tumor suppressor in lung cancer 1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NB1_TaxID-10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ;			
RA	Fukami T., Maruyama T., Murakami Y.;			
RL	"Identification of murine orthologue of the TSLC1 gene."			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBD databases.			
DR	EMBL: AF434663; AAL6736.1; -			
SQ	SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70H55 CRC64;			

Query Match	98.9%	Score 1741;	DB 11;	Length 445;
Best Local Similarity	98.8%	Pred. No. 1.8e-137;		
Matches 332; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible]

RESULT 3
Q8R5M8

ID	Q8R5M8	PRELIMINARY;	PRT;	456 AA.
AC	Q8R5M8:			
DT	01-JUN-2002 (TREMblrel_21, Created)			
DT	01-JUN-2002 (TREMblrel_21, Last annotation update)			
DT	01-JUN-2002 (TREMblrel_21, Last annotation update)			
DE	RA175.			
GN	RA175.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Momoi T.;			
RT	"Biological function of RA175, a new member of immunoglobulin super			
RT	family.";			
RL	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AB064265; BAB83501.2; -			
SO	SEQUENCE 456 AA; 45787 MW; 3226E866A4BC1C7F CRC64;			

Query Match	98.0%;	Score 1725.5;	DB 11;	Length 456;
Best Local Similarity	95.7%;	Pred. No. 3.7e-136;		
Matches 332;	Conservative 1;	Mismatches 3;	Indels 11;	Gaps 1;

QY	1	IPITGGQGNLFKRDVTVIEGEVAATISCOYKNSKDSVDVITOLMPNRQTIYFRPRPLKDSRFQ	60
Dd	42	IPITGGQGNLFKRDVTVIEGEVAATISCOYKNSKDSVDVITOLMPNRQTIYFRPRPLKDSRFQ	100
QY	61	LLNSSFSLKATSLINVSISDGRFCQLYDDPDESTTTTIVLPYPRNMIIDIOKTAVE	120
Dd	102	LLNSSFSLKATSLINVSISDGRFCQLYDDPDESTTTTIVLPYPRNMIIDIOKTAVE	160
QY	121	GEEIEVNTAMASKPATITIRMFKNFTELKSGEVEEWSMDYTVISQMLLVYKHEDDSVPV	180
Dd	162	GEEIEVNTAMASKPATITIRMFKNFTELKSGEVEEWSMDYTVISQMLLVYKHEDDSVPV	220
QY	181	ICQYEHNAVYNGNLTQRYLEYQYKRYOYNIQMTYRLOGSLTEBGDALETCSAIGKRPQVWY	240
Dd	222	ICQYEHNAVYNGNLTQRYLEYQYKRYOYNIQMTYRLOGSLTEBGDALETCSAIGKRPQVWY	280
QY	241	TWYRVDEDEMPQHNALVSGPNIETINNANKTDNGTYRCEASNTVGAHSDYMLUYVDDPTTIP	300
Dd	282	TWYRVDEDEMPQHNALVSGPNIETINNANKTDNGTYRCEASNTVGAHSDYMLUYVDDPTTIP	340
QY	301	PRTTTTTTTTTTTTTTTTITIT-----DSRAGEESGIRAVDH	360
Dd	342	PRTTTTTTTTTTTTTTTTITIT-----DSRAGEESGIRAVDH	380

RESULT 4	
Q9CRY3	
ID Q9CRY3	PRELIMINARY; PRT; 494 AA

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 3100000108RIK protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuda Y., Nikido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,
RA Wynchaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK013911; BAB29050.1; -
DR MGD: MGI:1889272; I9sf4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_3.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; IG_Like; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 494 AA; 53946 MW; F5E09ABA1857ABC0 CRC64;

Query Match 98.0%; Score 1725.5; DB 11; Length 494;
Best Local Similarity 95.7%; Pred. No. 4,1e-136;
Matches 332; Conservative 1; Mismatches 3; Indels 11; Gaps 1;

OY 1 IPTGDCQNLFTKDVNIEGEVATISCOVNSDSDSVIQLNPNRQTYFRDPRFLKDSRQ 60
DB 80 IPTGDCQNLFTKDVNIEGEVATISCOVNSDSDSVIQLNPNRQTYFRDPRFLKDSRQ 139
OY 61 LNFSSSELKSLTNVISDEGRYFCQLYTDPQESYTTITVLPVRNMLIDIOKTAVE 120
DB 140 LNFSSSELKSLTNVISDEGRYFCQLYTDPQESYTTITVLPVRNMLIDIOKTAVE 199
OY 121 GEEIENCTAMASKPATTTIRMFKNTELKSKSEVEEMSDMTYTTSOLMLKVHKEDGVPV 180
DB 200 GEEIENCTAMASKPATTTIRMFKNTELKSKSEVEEMSDMTYTTSOLMLKVHKEDGVPV 259
OY 181 ICVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTREGDALELTCGALGKPOPVNV 240
DB 260 ICVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTREGDALELTCGALGKPOPVNV 319
OY 241 TTVRVDDDEMPQAHVLSGPNLFINNLKKTNDNGTYRCASNIYVKAHSDYMLYVDPPTTIP 300
DB 320 TTVRVDDDEMPQAHVLSGPNLFINNLKKTNDNGTYRCASNIYVKAHSDYMLYVDPPTTIP 379
OY 301 PPTTTTTTTTTTTTTTTTTT-----DSRAGEGGSIRAVDH 336
DB 380 PPTTTTTTTTTTTTTTTTTT-----DSRAGEGGSIRAVDH 426

RESULT 5

09D6E7 PRELIMINARY: PRT; 336 AA.
AC 09D6E7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 2900073606R1K protein.
GN IGSF4 OR 2900073606R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid-10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,
RA Wynchaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK013775; BAB28988.1; -
DR MGD: MGI:1889272; I9sf4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_3.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; IG_Like; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 336 AA; 37157 MW; FF887FAF4EFD120 CRC64;

Query Match 86.8%; Score 1529; DB 11; Length 336;
Best Local Similarity 99.3%; Pred. No. 6.7e-120;
Matches 291; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 IPTGDCQNLFTKDVNIEGEVATISCOVNSDSDSVIQLNPNRQTYFRDPRFLKDSRQ 60
DB 42 IPTGDCQNLFTKDVNIEGEVATISCOVNSDSDSVIQLNPNRQTYFRDPRFLKDSRQ 101
OY 61 LNFSSSELKSLTNVISDEGRYFCQLYTDPQESYTTITVLPVRNMLIDIOKTAVE 120
DB 102 LNFSSSELKSLTNVISDEGRYFCQLYTDPQESYTTITVLPVRNMLIDIOKTAVE 161
OY 121 GEEIENCTAMASKPATTTIRMFKNTELKSKSEVEEMSDMTYTTSOLMLKVHKEDGVPV 180
DB 162 GEEIENCTAMASKPATTTIRMFKNTELKSKSEVEEMSDMTYTTSOLMLKVHKEDGVPV 221
OY 181 ICVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTREGDALELTCGALGKPOPVNV 240
DB 222 ICVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTREGDALELTCGALGKPOPVNV 281
OY 241 TTVRVDDDEMPQAHVLSGPNLFINNLKKTNDNGTYRCASNIYVKAHSDYMLYV 293
DB 282 TTVRVDDDEMPQAHVLSGPNLFINNLKKTNDNGTYRCASNIYVKAHSDYMLYV 334

RESULT 6

09Z2H8 PRELIMINARY: PRT; 295 AA.
AC 09Z2H8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Nectin-like protein 2.
GN IGSF4 OR NECTL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid-10090;
RN (1)
RP SEQUENCE FROM N.A.

RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.:
 "Cloning of a novel cDNA encoding a member of immunosuperfamily."
 RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF061260; AAC67243.1; -
 DR MGD: MGI:1889272; IgSF4.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00410; IG_Like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6488 CRC64;

Query Match 67.0%; Score 1180; DB 11; Length 295;
 Best Local Similarity 98.2%; Pred. No. 9.1e-91;
 Matches 223; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 110 MIDIQDTAVEGEIEVNCNTAMASKPATYIRWFGKNTLKGKSEVEEMSDMYTYSQML 169
 AC 09QYL6 PRELIMINARY; PRT; 306 AA.
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE Adhesion protein RAI75A.
 GN IGSP4 OR RAI75A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RT "RAI75, a novel neuron specific adhesion protein."
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AB021964; BAA87914.1; -
 DR MGD: MGI:1889272; IgSF4.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00410; IG_Like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;

QY 290 LYYVDPEPTTIPPTTT 336
 DB 181 LYYVDPEPTTIPPTTT 227

RESULT 7
 Q9QYL4 PRELIMINARY; PRT; 306 AA.
 ID 09QYL4
 AC 09QYL4
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE Adhesion protein RAI75C.
 GN IGSP4 OR RAI75C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RT "RAI75, a novel neuron specific adhesion protein."
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AB021966; BAA87916.1; -
 DR MGD: MGI:1889272; IgSF4.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00410; IG_Like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4CE37B0E23554D5 CRC64;

Query Match 65.7%; Score 1157.5; DB 11; Length 306;
 Best Local Similarity 93.3%; Pred. No. 7.3e-89;
 Matches 222; Conservative 2; Mismatches 3; Indels 11; Gaps 1;

QY 110 MIDIQDTAVEGEIEVNCNTAMASKPATYIRWFGKNTLKGKSEVEEMSDMYTYSQML 169
 DB 1 MIDIQDTAVEGEIEVNCNTAMASKPATYIRWFGKNTLKGKSEVEEMSDMYTYSQML 60
 QY 170 KVHKEDDGVVICOVEHPAVTGNLQOTRYLEVOYKRPVHIQMTYPIQGLTREGDALELTC 229
 DB 61 KVHKEDDGVVICOVEHPAVTGNLQOTRYLEVOYKRPVHIQMTYPIQGLTREGDALELTC 120
 QY 230 EAIGKPPVWTVWVRVDEMPQHAVALSGPNLFINNLTNGTYRCEASNIYGAHSDYM 289
 DB 121 EAIGKPPVWTVWVRVDEMPQHAVALSGPNLFINNLTNGTYRCEASNIYGAHSDYI 180
 QY 290 LYYVDPEPTTIPPTTT 336
 DB 181 LYYVDPEPTTIPPTTT 238

RESULT 8
 Q9QYL6 PRELIMINARY; PRT; 295 AA.
 ID 09QYL6
 AC 09QYL6
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE Adhesion protein RAI75A.
 GN IGSP4 OR RAI75A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RT "RAI75, a novel neuron specific adhesion protein."
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AB021964; BAA87914.1; -
 DR MGD: MGI:1889272; IgSF4.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00410; IG_Like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;

Query Match 64.6%; Score 1137; DB 11; Length 295;
 Best Local Similarity 94.7%; Pred. No. 3.6e-87;
 Matches 215; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 110 MIDIQDTAVEGEIEVNCNTAMASKPATYIRWFGKNTLKGKSEVEEMSDMYTYSQML 169
 DB 1 MIDIQDTAVEGEIEVNCNTAMASKPATYIRWFGKNTLKGKSEVEEMSDMYTYSQML 60
 QY 170 KVHKEDDGVVICOVEHPAVTGNLQOTRYLEVOYKRPVHIQMTYPIQGLTREGDALELTC 229
 DB 61 KVHKEDDGVVICOVEHPAVTGNLQOTRYLEVOYKRPVHIQMTYPIQGLTREGDALELTC 120
 QY 230 EAIGKPPVWTVWVRVDEMPQHAVALSGPNLFINNLTNGTYRCEASNIYGAHSDYM 289
 DB 121 EAIGKPPVWTVWVRVDEMPQHAVALSGPNLFINNLTNGTYRCEASNIYGAHSDYI 180
 QY 290 LYYVDPEPTTIPPTTT 336
 DB 181 LYYVDPEPTTIPPTTT 227

RESULT 9
 Q9QYL5 PRELIMINARY; PRT; 289 AA.
 ID 09QYL5

AC O90YL5:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RA175B.
GN IGSF4 OR RA175B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
RA Momoi T.;
RL "RA175, a novel neuron specific adhesion protein.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB021965; BAA87915.1; -;
DR MGI: 1889272; Igsf4.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00294; 4.Im. 1.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00410; IGC1like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 289 AA; 31811 MW; 801B836D0565AE4A CRC64;

Query Match 59.5%; Score 1048; DB 11; Length 289;
Best Local Similarity 89.4%; Pred. No. 9.9e-80;
Matches 203; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

OY 110 MIDICKDTAVEGEELVENCNTAMASKPATITRMFKGNTLKGSEVEWSDMTVTYSQML 169
DB 1 MIDICKDTAVEGEELVENCNTAMASKPATITRMFKGNTLKGSEVEWSDMTVTYSQML 60
OY 170 KVKHEDDGVYVICOVENHRAVNTGNLQRYLEYQKPOVHIQMTYPLQGLTRGDALELTC 229
DB 61 KVKHEDDGVYVICOVENHRAVNTGNLQRYLEYQKPOVHIQMTYPLQGLTRGDALELTC 120
OY 230 EAIGKPOVMTWVRVDDMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYGAHSDYM 289
DB 121 EAIGKPOVMTWVRVDDMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYGAHSDYI 180
OY 290 LVYDPEPTTIPPTTTTTTTTTTTTTLTIITDSRAGEGSIKAVDH 336
DB 181 LVYDPTTTT-----LTITDTTATTEPAVHDSRAGEGSIKAVDH 221
RESULT 10
O90YL3
ID O90YL3 PRELIMINARY: PRT: 278 AA.
AC O90YL3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RA175N.
GN IGSF4 OR RA175N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
RA Momoi T.;
RL "RA175, a novel neuron specific adhesion protein.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB021967; BAA87917.1; -;
DR MGI: 1889272; Igsf4.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_1like.

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00294; 4.Im. 1.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00410; IGC1like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;

Query Match 58.2%; Score 1024.5; DB 11; Length 278;
Best Local Similarity 87.2%; Pred. No. 8.7e-78;
Matches 198; Conservative 3; Mismatches 9; Indels 17; Gaps 1;

OY 110 MIDICKDTAVEGEELVENCNTAMASKPATITRMFKGNTLKGSEVEWSDMTVTYSQML 169
DB 1 MIDICKDTAVEGEELVENCNTAMASKPATITRMFKGNTLKGSEVEWSDMTVTYSQML 60
OY 170 KVKHEDDGVYVICOVENHRAVNTGNLQRYLEYQKPOVHIQMTYPLQGLTRGDALELTC 229
DB 61 KVKHEDDGVYVICOVENHRAVNTGNLQRYLEYQKPOVHIQMTYPLQGLTRGDALELTC 120
OY 230 EAIGKPOVMTWVRVDDMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYGAHSDYM 289
DB 121 EAIGKPOVMTWVRVDDMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYGAHSDYI 180
OY 290 LVYDPEPTTIPPTTTTTTTTTTTTTLTIITDSRAGEGSIKAVDH 336
DB 181 LVYD-----TTATTEPAVHDSRAGEGSIKAVDH 210

RESULT 11
O9R464
ID O9R464 PRELIMINARY: PRT: 388 AA.
AC O9R464:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Membrane glycoprotein.
GN TSL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Matuyama T., Murakami Y.;
RL "Identification of a murine ortholog of the TSLC1-like gene 2.";
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY059394; AAL29692.1; -;
SQ SEQUENCE 388 AA; 42723 MW; 8E3A9DF1C3B9D23E CRC64;

Query Match 35.3%; Score 622; DB 11; Length 388;
Best Local Similarity 40.6%; Pred. No. 6.6e-44;
Matches 123; Conservative 62; Mismatches 112; Indels 6; Gaps 3;

OY 4 GGGONLFTDMVTVIEGEVATISCOVKKSDPSYIQLNPNKOTYFRDFPKDPSRQLLN 63
DB 22 GTGQEVQTEVNTVVAEGVAETICRLHNDGSIYVIONPAROTLFFNGTALAKDERQLEB 81
OY 64 FSSSELKAVSLTVNSISDEGRFCOLYTDPRQESYTTTVLVPRNLMIDICKDTAVEGEE 123
DB 82 FSPRRVRIKRLSDARLEDEGFCOLYTEDTHNQIATLVLAPEENLVVEV-RQAQVEGG 140
OY 124 IEVNCNTAMASKPATITRMFKGNTLKGSEVEWSDMTVTYSQMLKVKHEDDGVYVICO 183
DB 141 VELSCVLPRSPRAVALRWYRDRKELKGVSSQGENGVWVASVSTRVVRKDDGGIVICE 200
OY 184 VEHRAVTTG--NIQTORLEYQKPOVHIQMTYPLQGLTRGDALELTCGAKPOPVMT 241
DB 201 AQNGALPSGHSKQTVLVLDVQYSPTARIHAS---QAVAREGDTLVLTCAVTAQVPRNQIR 257
OY 242 WVRVDDMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYGAHSDYMLVYDPTTIP 301

DB 258 WNRGNESLPERAEVGETLTLPGLVSADNGTYTCEANKHGHRALYLVLYVDPGAVEEA 317
QY 302 PTT 304
DB 318 QTS 320

RESULT 12

QY4A4 ID QY4A4 PRELIMINARY; PRT; 381 AA.
AC 09Y4A4
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F22162.1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhart-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 2.5 Mb region in 19q13.2 containing a
RT clustered CEAPSG gene family";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005525; AAC32740.1; -
DR HSSP; P80748; 2IOT.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00294; 4.Im; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IGC1-like; 2.
KW Immunoglobulin domain.
FT NON_TER
SQ SEQUENCE 381 AA; 4187 MW; 315420B36FBFDC05 CRC64;

Query Match

Best Local Similarity 39.1%; Score 609; DB 4; Length 381;
Matches 126; Conservative 62; Mismatches 120; Indels 14; Gaps 5;

QY 6 GONLFTKDYTVIEGEVATISCOYKNSDSDSVIQLLPNROTIYFRDRPLKDSRFOLLNF 65
DB 2 GGEVQENTVTAEGVAELTCRLHGYDGSIVIQNPARTLPFGNTRALKDEFQLEERS 61
QY 66 SSELKVSILTNVISIDEGRYFCOLYDPPQESYTTITVLVPPRLMIDIOKTAVEGEET 125
DB 62 PRVRIRLSDARLEDEGEGYFCOLYEDTHHQJATLTLVLAPEPNVVEV-REQVEGGEVE 120
QY 126 VNCSTAMASRPATTIRFKNTKELKSEVEEWSDMATVTISQMLKVKHEDDGVPIQYVE 185
DB 121 LSCVLPSPRSPATLRWYRDRKELKGVSSQENKGVMSVASTVFRDRKDDGIIICEAQ 180
QY 186 HPAVING-NLQOTRYLEYQYKRPVNHQMTYPLQGLTRREDALELTCEALGKPPQVNTWY 243
DB 181 NQALPSGSHKQYQYVLDVQYSPARIHAS---QAVVREGDVLVLTCAVTGNPPRNQIRVN 237
QY 244 RYDDEMPQHAVISGPNLFTNNLNKTDNGTYRCEASNIYVKAHSDYLYYDP-----PTT- 298
DB 238 RGNESLPERAEVGETLTLPGLVSADNGTYTCEASNKHGHRALYLVLYVYGESRLRPTGS 297
QY 299 ---IPPTTTTTTTTTTTTTTTTIL 317

DB 298 GGGAPDPGAVEAQTSPVPAIV 319

RESULT 13

QY9N28 ID QY9N28 PRELIMINARY; PRT; 396 AA.
AC 099N28
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein).
GN NECT1 OR TSL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RT "Cloning and expression analysis of novel mouse cDNA encoding a
RT membrane protein";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of a murine ortholog of the TSLC1-like gene 1";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A195662; AAG35584.1; -
DR EMBL; A1059393; AAL28691.1; -
DR MGD; MGI:2137858; Nect1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00410; IGC1-like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 396 AA; 42964 MW; C1ADF8B57D141F3A CRC64;

Query Match

Best Local Similarity 35.4%; Score 482.5; DB 11; Length 396;
Matches 110; Conservative 63; Mismatches 119; Indels 19; Gaps 7;

QY 5 DGNLFTKDYTVIEGEVATISCOYKNSDSDSVIQLLPNROTIYFRDRPLKDSRFOLLNF 64
DB 27 DDSQPTISDETVAAGTVAALKCVKDHEDSSLSQWNPAAQOTLYFGKRALDRNRQLVSS 86
QY 65 SSELKVSILTNVISIDEGRYFCOLYDPPQESYTTITVLVPPRLMIDIOKTAVEGEET 124
DB 87 TRHELISISNVALADEGETCSITFMPVPTASLTVLGIPKPIITTKSSLRKRETA 146
QY 125 EVNCTAMASRPATTIRFKNTKELK-KSEVEEWSM-D-NYTVTSQMLKVKHEDDGVPI 181
DB 147 TLNCSGSSGKPAQALFWRRGDQELHGDQFRIOEDPDKTFYVSSVSFQVTRREDGANIV 206
QY 182 CQVEHPAVING-NLQOTRYLEYQYKRPVNHQMTYPLQGLTRREGALTEALGKPPQVNTW 240
DB 207 CSVNHESLGADPSTQSRLEVLTPYAMIR--PEPAHPRREGQKLLHCEGRGNPVPQY 263
QY 241 TWVRVDDEMP---QHAVISGPNLFTNNLNKTDNGTYRCEASNIYVKAHSDYLYYDDP 296
DB 264 VVWKESSEPLKMTQESALIFP-----FLNKSDSGTYGCTATYSNMGSYTAFFTLNVNDS 318
QY 297 TTIPPTTTTT 307
DB 319 ---PVPSSST 326

RESULT 14

Q9UJPI

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OM nucleic - protein search, using frame_plus.n2p model

Run on: November 20, 2002, 07:46:46 ; Search time 17.5 Seconds
(without alignments)
3389.521 Million cell updates/sec

Title: US-09-778-187b-3_COPY_62_1069

Perfect score: 1804

Sequence: 1 atcccacaggtgacgacac.....ccattgggagcgctgaccac 1008

Scoring table:

	BLOSUM62
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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_AA -QPMF=fastan -SUFFIX=rai -MINMATCH=0.1 -IOOFCI=0
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-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625.5	34.7	421	2	US-08-659-984A-1
2	625.5	34.7	421	2	US-08-660-531-1
3	625.5	34.7	444	4	US-08-659-984A-5
4	625.5	34.7	444	4	US-08-660-531-5
5	321	12.8	393	1	US-08-429-742-2
6	207	11.5	458	4	US-09-433-956A-1
7	204.5	11.3	388	1	US-08-429-742-4
8	204	11.3	642	1	US-08-217-299-1
9	204	11.3	698	2	US-08-602-725-36
10	204	11.3	734	2	US-08-389-459A-17
11	204	11.3	734	3	US-08-987-867A-17
12	193	10.7	1395	4	US-09-540-245A-15

13	192	10.6	1651	4	US-09-540-245A-18	Sequence 18, Appl
14	191.5	10.6	583	2	US-08-432-016-2	Sequence 2, Appl
15	191.5	10.6	583	2	US-08-684-594-2	Sequence 2, Appl
16	187.5	10.4	308	2	US-08-414-657D-46	Sequence 46, Appl
17	187.5	10.4	325	2	US-08-414-657D-2	Sequence 2, Appl
18	187.5	10.4	325	2	US-08-414-657D-41	Sequence 41, Appl
19	187.5	10.4	325	4	US-09-135-080-2	Sequence 2, Appl
20	187	10.4	287	2	US-08-414-657D-48	Sequence 48, Appl
21	187	10.4	304	2	US-08-414-657D-44	Sequence 44, Appl
22	187	10.4	477	2	US-08-432-016-3	Sequence 3, Appl
23	187	10.4	477	2	US-08-684-594-3	Sequence 3, Appl
24	185.5	10.3	315	2	US-08-414-657D-47	Sequence 47, Appl
25	185.5	10.3	338	2	US-08-414-657D-42	Sequence 42, Appl
26	185.5	10.3	338	2	US-08-414-657D-43	Sequence 43, Appl
27	185.5	10.3	338	4	US-09-135-080-4	Sequence 4, Appl
28	185.5	10.3	1241	4	US-09-040-774-2	Sequence 2, Appl
29	185	10.3	287	2	US-08-414-657D-49	Sequence 49, Appl
30	185	10.3	310	2	US-08-414-657D-45	Sequence 45, Appl
31	183.5	10.2	1297	4	US-09-540-245A-17	Sequence 17, Appl
32	181.5	10.1	1447	4	US-09-041-886-25	Sequence 25, Appl
33	181.5	10.1	1447	5	PCT-US94-05277-2	Sequence 2, Appl
34	179.5	10.0	338	2	PCT-US94-05277-2	Sequence 60, Appl
35	179.5	10.0	338	4	US-09-135-080-8	Sequence 8, Appl
36	174.5	9.7	478	5	PCT-US95-08493-15	Sequence 15, Appl
37	174.5	9.7	860	5	PCT-US95-08493-19	Sequence 19, Appl
38	174.5	9.7	868	5	PCT-US95-08493-21	Sequence 21, Appl
39	173.5	9.6	408	4	US-09-724-864-62	Sequence 62, Appl
40	172.5	9.6	869	1	US-08-374-834-16	Sequence 16, Appl
41	172.5	9.6	869	2	US-08-644-271-29	Sequence 29, Appl
42	172.5	9.6	869	4	US-09-077-955-33	Sequence 33, Appl
43	172	9.5	607	2	US-08-752-307B-12	Sequence 12, Appl
44	172	9.5	607	4	US-09-707-802-12	Sequence 12, Appl
45	172	9.5	607	4	US-09-991-326-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:46:20 ; Search time 39.5 seconds

(without alignments)
4906.506 Million cell updates/sec

Title: US-09-778-187B-3_COPY_62_1069

Perfect score: 1604

Sequence: 1 atccacagatgagtgacac.....ccattgggagcgtgaccac 1008

Scoring table: BIOSUM62

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Xgapop 10.0 , Ygapext 0.5

Xgapop 6.0 , Ygapext 7.0

Delop 6.0 , Delext 7.0

Searched: 263224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=45

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-WALL_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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4	238	13.2	725	2	J60099
5	234	13.0	1088	1	IYX1ML
6	228.5	12.7	7962	2	I38346
7	226	12.5	4162	2	T42633
8	223	12.4	344	2	I56551
9	222	12.3	530	2	A53437
10	222	12.3	725	2	J60100
11	222	12.3	1092	1	JN0635
12	221.5	12.3	538	2	I68093
13	220	12.2	392	2	B4194
14	220	12.2	417	2	A4194

15	220	12.2	467	1	HLKSP3	poliovirus recepto
16	218	12.1	392	1	RWHUPD	poliovirus recepto
17	218	12.1	417	1	RWHUPD	poliovirus recepto
18	216.5	12.0	478	2	I53960	PR2 alpha - human
19	216	12.0	4391	2	A38096	perlecan precursor
20	214	11.9	1011	2	T13669	neuromusculin - fr
21	210	11.6	518	2	JC4024	poliovirus recepto
22	209.5	11.6	345	2	S03199	oploid-binding pro
23	209.5	11.6	584	2	I50419	s-glycerin precurs
24	207.5	11.5	345	2	JC4025	oploid-binding cel
25	206.5	11.4	862	2	I49583	differentiation an
26	206.5	11.4	868	2	A46512	CD22 homolog/B lym
27	206	11.4	847	2	JH0371	B-cell adhesion pr
28	205.5	11.4	812	2	B42632	cell adhesion mole
29	205.5	11.4	932	2	A42632	cell adhesion mole
30	204	11.3	702	2	A36319	carcinoembryonic a
31	202	11.2	1443	2	I50600	neogenin - chicken
32	201.5	11.2	345	2	JC1239	oploid-binding pro
33	200.5	11.1	338	2	JC1238	oploid-binding pro
34	199	11.0	338	2	JC5519	50K glycoprotein p
35	195.5	10.8	765	2	C42632	cell adhesion mole
36	195	10.8	1344	2	T14316	rig-1 protein - mo
37	194.5	10.8	3707	2	S18252	heparan sulfate pr
38	193	10.7	588	2	A45234	surface glycoprote
39	193	10.7	761	1	I4HUNG	neural cell adhesi
40	193	10.7	1091	1	ITCHNL	neural cell adhesi
41	193	10.7	1323	2	PN0568	connectin 3B - chi
42	193	10.7	1612	2	T30805	ducl1 protein - mo
43	192	10.6	1036	2	S22383	axonin 1 precursor
44	191.5	10.6	583	2	I39428	alcam - human
45	190	10.5	646	2	I38049	cell surface glyco

ALIGNMENTS

RESULT 1

T20992 hypothetical protein F15G9.4a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T20992; T24733

R:Suiston, J.

submitted to the EMBL Data Library, December 1994

A:Reference number: Z19355

A:Accession: T20992

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5175 <WIL>

A:Cross-references: EMBL:Z47070; PIDN:CA87335.1; GSPDB:GN00028; CESP:F15G9.4a

A:Experimental source: clone F15G9

R:Kershaw, J.

submitted to the EMBL Data Library, December 1994

A:Reference number: Z19929

A:Accession: T24733

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5175 <WIL>

A:Cross-references: EMBL:Z47070; PIDN:CA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A:Experimental source: clone T09B9	
C:Genetics:	
A:Gene: CESP:F15G9.4a	
A:Map position: X	
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/1; 2512/3; 2593/3; 2699/3; 2759/1; 2852/1; 2869/3; 2913/3; 2941/1; 2967/3; 2991/3; 303/1; 4225/1; 4361/1; 4408/1; 4456/1; 4496/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 50	
Alignment Scores:	
Pred. No.:	4.16e-12
Score:	261.50
Percent Similarity:	43.06%
Best Local Similarity:	24.65%
Query Match:	14.50%
DB:	2
Length:	5175
Matches:	87
Conservative:	65
Mismatches:	130
Indels:	71
Gaps:	15

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US-09-778-187B-3_COPY_62_1069 (1-1008) x T20992 (1-5175)
QY 40 GTGACAGTATGTAAGAGTGCACACCATGATGCGCATTAAGAGTGCAC 99
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2200 ValThAlaIleYsGlyAlaLeuProPhelyCysProIleSp-----AspSp 2217
QY 100 TCAGTATCCAGCTCTGAACCCCAACAGCAGACCATTTACTTCAAGGACTTCAAGCCT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2218 Lys-----AsnPhelySGlyGlnIleIleThrePneurYgAsnTyGlnPro 2232
QY 160 TTG-----AAGCAGCAGAGTTTCACTGCTGAATTTTCTACAGTGAAC 207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2233 IleAspLeuGlnAlaGlnAspAlaArgIleThrArgLeu-----SerAsnAspArg 2249
QY 208 AAGGTCACTGACGAGTATGCTCAATCTGATGAGGAGGAGTACTTCTCCAGCTTAC 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2250 ArgLeuThrIleLeuAsnValThrGlnAsnAspGlnGlnTySerCysArgValLys 2269
QY 268 ACGGACCCCCACAGAGAGATTACACC--ACCATCAGACTCTGCTTCTCCAGCTTAC 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2270 AsnAspAlaGlyGlnAsnSerPheAspPhelyAlaThrValLeuValProProthIle 2289
QY 325 TTGATATGATATCCAGAAAGAC---ACGGCAGTTGAGGAGGAGAGATTTGAGTCAAC 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2290 IleMetLeuAspLysAspLysAsnLysThrAlaValGlnHisSerThrValThrLeuSer 2309
QY 382 TGTACTGATGCGCAGCAGACGACGACGACGATGAGGTGCTTCAAGG----- 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2310 CysProAla---ThrGlyLysProGlnProAspIleThrThrPhelysAspGlyGlnAla 2328
QY 433 -----ACAGAGCACTCAAGCAAGCAATCAGAG 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2329 IleHisIleGlnAsnIleAlaAspIleIleProAsnGlnGlyLeuAsnGly----- 2445
QY 460 GTGAGAGAGTGGTGGCAGCATGTACTGTGACCATGCTGCTGCTGAAGGTGCACAG 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2346 -----AsnGlnLeuLysIleThrArgIleLys 2354
QY 520 GAGGACGAGGGGGTCCCGGTGATGTCGCAAGTGAGCAGCCCTGCGTCACTGCAAACTG 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2355 GlnGlyAspAlaGlyLysTyThrCysGlnAlaAspAsnSerAla-----GlySerVal 2372
QY 580 CAGACCCAGCGCTATCTAGAGTCAAGTAAACCCGCAAGTGCAT-----ATCCAG 630
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2373 GlnGlnAspValAsnValAsnValIleThrIleProLysIleGlnLysAspGlyIlePro 2392
QY 631 ATGACTTACCTCTGCAAGCCCTAACCCGGAAGGGGAGCATTTAGTTAAGTGTGA 650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2393 SerAspTyGlnSerGln-----GlnAsnGlnArgValValIleSerCysPro 2408
QY 691 GCCATGGGAGAGCCCGCTGATGTAACCTTGGGTGAGATGCGATGATGAATAGCCCT 750
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2409 ValTyAlaArgPro---ProAlaLysIleThrThrePneulysAlaLysProLeuGln 2427
QY 751 CAACATCCGCTACTG-----TCTGGCCAAACCTGTTCATCAATAAAGCTAAAC 798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2428 SerAspLysPheValIleThrSerAlaAsnGlnGlnLysLeuThrePneulysLeuArg 2447
QY 799 AAACAGATTAAGGTTACTTACCCCTGTAAGCCTTCAACATAGTGGGAAGGCTCATTCG 858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2448 GlnThAspSerSerLysTyThrCysIleAlaThAsnGlnAlaGlyThAspLysArg 2467
QY 859 GATTATATCTGATATACGATCCCGCCACCAATATCCCTCCCT----- 903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2468 AspPhelyValSerMetLeuValAlaProSerPheAspGlnProAsnIleValAlaArg 2487
QY 904 -----CCACACACACACACACACACACACACACACACACACACACACAC 942
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2488 IleThValAsnSerGlnAsnProSerThreLueHisCysProAlaLysGlySerProSer 2507
QY 943 ACCATCTTACCATCATCATCTCGACGAGGTGA 981
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Db 2508 ProThrIleThrThrePneulysAspGlyAsnAlaIleGln 2520
RESULT 2
T43290
hemiscetin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43290; T20993; T24734
R:Voegel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A:Description: Hemiscetin is required for hemidesmosome mediated cell adhesion and ge
A:Reference number: Z22396
A:Accession: T43290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5198 <V06>
A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20993
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <W11>
A:Cross-references: EMBL:247068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:FL1569.4b
A:Experimental source: clone F1569
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <W12>
A:Cross-references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:FL1569.4b
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F1569.4b
A:Map position: x
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184
1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 51
Alignment Scores:
Pred. No.: 4.16e-12 Length: 5198
Score: 261.50 Matches: 87
Percent Similarity: 43.06 Conservative: 65
Best Local Similarity: 24.65 Mismatches: 130
Query Match: 14.508 Indels: 71
DB: Gaps: 15
US-09-778-187B-3_COPY_62_1069 (1-1008) x T43290 (1-5198)
QY 40 GTGACAGTATGTAAGAGTGCACACCATGATGCGCATTAAGAGTGCAC 99
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2200 ValThAlaIleYsGlyAlaLeuProPhelyCysProIleSp-----AspSp 2217
QY 100 TCAGTATCCAGCTCTGAACCCCAACAGCAGACCATTTACTTCAAGGACTTCAAGCCT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2218 Lys-----AsnPhelySGlyGlnIleIleThrePneurYgAsnTyGlnPro 2232
QY 160 TTG-----AAGCAGCAGAGTTTCACTGCTGAATTTTCTACAGTGAAC 207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2233 IleAspLeuGlnAlaGlnAspAlaArgIleThrArgLeu-----SerAsnAspArg 2249
QY 208 AAGGTCACTGACGAGTATGCTCAATCTGATGAGGAGGAGTACTTCTCCAGCTTAC 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2250 ArgLeuThrIleLeuAsnValThrGlnAsnAspGlnGlnTySerCysArgValLys 2269
QY 268 ACGGACCCCCACAGAGAGATTACACC--ACCATCAGACTCTGCTTCTCCAGCTTAC 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2270 AsnAspAlaGlyGlnAsnSerPheAspPhelyAlaThrValLeuValProProthIle 2289
QY 325 TTGATGATGATATCCAGAAAGAC---ACGGCAGTTGAGGAGGAGATTTGAGTCAAC 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus.n2p model

Run on: November 20, 2002, 07:40:00 ; Search time 15.5 Seconds
(without alignments)
5394.599 Million cell updates/sec

Title: US-09-778-187b-3_COPY_62_1069
Perfect score: 1804
Sequence: 1 atcccccacagtgatgacac.....ccattggggcagtgaccac 1008

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p model -DEV=xlp
-Q=/cgn2.1/SPRO_gpcop/US9778187/runat_20112002_073629_26309/app_query.fasta.1.2318
-DB=SwissProt_40 -OPMT=fastan -SUFFIX=isp -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIG=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=tbl -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US9778187.ecgn.1.1.45.runat.20112002_073629_26309 -NCPI=6 -ICPU=3
-NO_XLPY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	13.0	1088	1	NCAL_XENLA
2	226.5	12.6	515	1	PVR1_PIG
3	225.5	12.5	837	1	NCM2_MOUSE
4	223	12.4	344	1	NR1_RAT
5	222	12.3	530	1	PVR2_MOUSE
6	222	12.3	1092	1	NCAL_XENLA
7	221.5	12.3	538	1	PVR2_HUMAN
8	220	12.2	337	1	G55A_CHICK
9	220	12.2	417	1	PVR_CERAE
10	218.5	12.1	517	1	PVR1_HUMAN
11	217	12.0	417	1	PVR_HUMAN
12	215.5	11.9	837	1	NCM2_HUMAN
13	215	11.9	4393	1	PCBM_HUMAN
14	211	11.7	847	1	CD22_HUMAN
15	209.5	11.6	345	1	OPCM_BOVIN
16	209	11.6	1242	1	NRPN_MOUSE
17	208.5	11.6	353	1	CEPU_CHICK
18	207.5	11.5	345	1	OPCM_HUMAN

19	207	11.5	1493	1	NEOL_MOUSE	P97798 mus musculus
20	206.5	11.4	862	1	CD22_MOUSE	P35329 mus musculus
21	204	11.3	702	1	CEA5_HUMAN	P06731 homo sapien
22	203	11.3	1461	1	NEOL_HUMAN	O92859 homo sapien
23	202	11.2	515	1	PVR1_HUMAN	O914f6 mus musculus
24	202	11.2	1443	1	NEOL_CHICK	O90610 gallus gall
25	201.5	11.2	345	1	OPCM_RAT	P32736 rattus norv
26	199	11.0	338	1	LAMP_CHICK	O98919 gallus gall
27	198	11.0	1377	1	NEOL_RAT	P97603 rattus norv
28	197	10.9	583	1	C166_MOUSE	O61490 mus musculus
29	194.5	10.8	3707	1	PCBM_MOUSE	O05793 mus musculus
30	194	10.8	1091	1	NCAL_CHICK	P13590 gallus gall
31	193	10.7	761	1	NCAL_HUMAN	P13592 gallus gall
32	193	10.7	848	1	NCAL_HUMAN	P13592 homo sapien
33	192	10.6	1036	1	AXOL_CHICK	P28685 gallus gall
34	191.5	10.6	583	1	C166_HUMAN	O13740 homo sapien
35	190.5	10.6	1447	1	DCG_MOUSE	P70211 mus musculus
36	190	10.5	646	1	MU18_HUMAN	P43121 homo sapien
37	189	10.5	853	1	NCAL_BOVIN	P31836 bos taurus
38	189	10.5	858	1	NCAL_RAT	P13596 rattus norv
39	188	10.4	388	1	C166_CHICK	P42292 gallus gall
40	187.5	10.4	338	1	LAMP_CHICK	O13449 homo sapien
41	185.5	10.3	338	1	LAMP_RAT	O62813 rattus norv
42	185.5	10.3	764	1	ICCR_DROME	O08180 drosophila
43	185.5	10.3	1234	1	NRPN_RAT	O91044 rattus norv
44	185.5	10.3	1241	1	NRPN_HUMAN	O60500 homo sapien
45	182.5	10.1	2012	1	DSCA_HUMAN	O60469 homo sapien

ALIGNMENTS

RESULT 1

NCAL_XENLA STANDARD: PRT: 1088 AA.

AC P16170;
DT 01-APR-1990 (rel. 14, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180).
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90098871; PubMed=2481269;
RA Kriegl P.A., Sakaguchi D.S., Kintner C.R.;
RT "Primary structure and developmental expression of a large cytoplasmic domain form of Xenopus laevis neural cell adhesion molecule (NCAM)."
RT Nucleic Acids Res. 17:10321-10335(1989).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: N-CAM 180 (shown here) and N-CAM 140; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL TISSUE.
CC -1- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:56:11 : Search time 8.5 Seconds
(without alignments)
3714.538 Million cell updates/sec

Title: US-09-778-187B-3_COPY_62_1069

Perfect score: 1804
Sequence: 1 atccacacagtgatgacac.....ccattggggcagtgaccac 1008

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 200960

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPRO_SPOOL/US09778187/runat_20112002_073633_26418/app.query.fasta.1.2318
-DB=Published_Applications_AA -OPMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09778187.ecgn.1.1.16 @runat.20112002_073633_26418
-NCPU=6 -ICPU=3 -NO_XLPHY -LARGEOUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA:*

- 1: /cgn2.6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
- 2: /cgn2.6/ptodata/1/pubpaa/PCRT_NEM_PUB.pep.*
- 3: /cgn2.6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
- 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2.6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
- 6: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2.6/ptodata/1/pubpaa/PCRTUS_PUBCOMB.pep.*
- 8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2.6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
- 10: /cgn2.6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2.6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
- 12: /cgn2.6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2.6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*
- 14: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	97.8	423	9	US-09-778-510-22 Sequence 22, Appl
2	1765	97.8	423	9	US-09-778-187B-4 Sequence 4, Appl
3	1741	96.5	440	9	US-09-944-413-61 Sequence 61, Appl
4	1741	96.5	440	9	US-09-944-403-61 Sequence 61, Appl

5	1741	96.5	440	9	US-09-944-896-61	Sequence 61, Appl
6	1741	96.5	440	10	US-09-866-028-61	Sequence 61, Appl
7	1741	96.5	440	10	US-09-944-449-61	Sequence 61, Appl
8	1741	96.5	440	10	US-09-944-457-61	Sequence 61, Appl
9	1741	96.5	440	10	US-09-944-862-61	Sequence 61, Appl
10	1741	96.5	440	10	US-09-945-587-61	Sequence 61, Appl
11	1741	96.5	440	10	US-09-945-015-61	Sequence 61, Appl
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18	1741	96.5	440	12	US-10-052-586-34	Sequence 34, Appl
19	1741	96.5	442	9	US-09-778-510-20	Sequence 20, Appl
20	1741	96.5	442	9	US-09-778-187B-2	Sequence 79, Appl
21	480.5	26.6	398	9	US-10-047-542-79	Sequence 4, Appl
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24	469.5	26.0	398	9	US-09-778-510-6	Sequence 10, Appl
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28	469.5	26.0	398	10	US-09-778-510-2	Sequence 8, Appl
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37	209	11.6	1256	9	US-10-047-542-90	Sequence 80, Appl
38	208	11.5	626	9	US-10-047-542-80	Sequence 794, App
39	207.5	11.5	550	10	US-09-764-853-794	Sequence 605, App
40	207	11.5	749	10	US-09-756-851A-17	Sequence 17, Appl
41	204	11.3	737	10	US-09-925-301-1133	Sequence 1133, Ap
42	203	11.3	350	9	US-09-808-602-71	Sequence 71, Appl
43	198	11.0	582	9	US-09-736-457-334	Sequence 334, App
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ALIGNMENTS

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Sequence 22, Application US/09778510
Patent No. US20020164686A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778, 510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCY/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095, 663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-22

Alignment Scores:
Pred. No.: 1.31e-115
Score: 1765.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 97.84%
Length: 423
Matches: 336
Conservative: 0
Mismatch: 0
Indels: 0

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/	TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM			
/	FILE REFERENCE: 2873-US			
/	CURRENT APPLICATION NUMBER: US/09/778,187B			
/	PRIOR FILING DATE: 2001-02-06			
/	PRIOR APPLICATION NUMBER: PCT/US99/17905			
/	PRIOR FILING DATE: 1999-08-05			
/	PRIOR APPLICATION NUMBER: US 60/095,672			
/	PRIOR FILING DATE: 1998-08-07			
/	NUMBER OF SEQ ID NOS: 10			
/	SOFTWARE: PatentIn version 3.1			
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/	ORGANISM: mus musculus			
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	Best Local Similarity: 100.00%		Mismatches: 0	
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Db 221 VALGINTYFLYBROGIVNVAHISLEGIMETHTYPROEUDINGLYEUTHFATG 240
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Sequence 61, Application US/09944413
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gertsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Auelin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
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PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: 60/069,702
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PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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: PRIOR APPLICATION NUMBER: PCT/US00/05841
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: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
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: ORGANISM: Homo Sapien
US-09-944-403-61
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: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Baton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavio, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944, 896
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866, 028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/069, 334
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 ? PRIOR FILING DATE: February 9, 1998
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 ? PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
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 ? PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
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 ? PRIOR FILING DATE: February 28, 2001
 ? NUMBER OF SEQ ID NOS: 120
 ? SEQ ID NO 61
 ? LENGTH: 440
 ? TYPE: PRT
 ? ORGANISM: Homo Sapien
 US-09-944-896-61

Alignment Scores: 6,11e-114 Length: 440
 Pred. No.: 1741.00 Matches: 332
 Score:

Percent Similarity: 99.11% Conservative: 1
 Best Local Similarity: 98.81% Mismatches: 3
 Query Match: 96.51% Indels: 0
 DB: 9 Gaps: 0
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 Db 177 TRPHELYSGLYASNTHRGILEULYSGLYLSERGLVALGLUGLUTRPSERASPME 196
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 QY 481 TNCAGTGTACCCAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 540
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 Db 197 TYRTHVALTHSERGLNLEUMETLULYSVALHISLYSGILNLSPPGLVALPROVAL 216
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 QY 541 ACTGCCACAGTGTGAGCACCCTGGCTCACTGCAACCTCCAGACCCAGCGCTATCTAGA 600
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 Db 217 IIECYGLINVALGLINHSIROALAVALTINGLYASNLEUGLINTHRLINRGYRLEUGLU 236
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 QY 601 TGCAGTATTAACCCGCAAGTGCATATCCAGATGACTTACCCTTCGACAGGCTAACCCG 660
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 Db 237 VALGLINTLYSPROGLINVALHISILEGLINMETHTYRPROLEUGLNGLYLEUTHRARG 256
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 QY 661 GAAGGGATGCACTTGTAGTTAAGTGTGAAGCCATGCGGAGAGCCCGACCTGTAGATGA 720
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 Db 257 GUGLYASPALALEUENLIEUTHRYCSGLUALALIEGLYLYSPROGLINPROVALMETVAL 276
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 QY 721 ACTTGGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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 Db 277 THRTPRVALARGVALASPSRGLUMETPROGLINHISALVALLEUSERTGLYPROASNLEU 296
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 QY 781 TTTATCAATTAACCTTAACAACAACAGATAAGGTACTTACCGCTGTGAGGCTTCCAACATA 840
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 Db 297 PHEILEASNASNLEULSNLYSTRASPASNGLYTHRYARGCYSGLNLSERASNILE 316
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 QY 841 GTGGGAAGGCTCATTTGGCATATATGCTGATGATGATGATGATGATGATGATGATGATG 900
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 Db 317 VALGLYLYSALANHSERASPRTYRMELEUTYRVALTYRASPPTROTHRTIRILEPRO 336
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 QY 901 CCTCCCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 960
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 Db 337 PROPTOTHT 356
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 QY 961 ACAGATTTCTGAGCAGGTGAGAGGAGGACCATTTGGGCGACGTGACAC 1008
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Db 357 ThrAspSerArgAlaGlycIuGlySerIleArgAlaValAspHis 372

RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botsstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Alignment Scores:
Pred. No.: 6,11e-114 Length: 440
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
Gaps: 0
DB: 10

US-09-778-187b-3_COPY_62_1069 (1-1008) x US-09-866-028-61 (1-440)

QY 1 ARCCCAAGCGATGAGCAATCGTTTACTAAAGAGCTGACAGCTGATTCAGAGAGAA 60
Db 37 lIeProThrGlyAspGlycIuAsnLeuPheThrLysAspValThrValIleGluGlyGlu 56
QY 61 GTGGCAACCATCAGGTGCGCAGGTCAATAAGAGTGAAGTCAAGTCAAGTCCAGGCTCGAAC 120
Db 57 ValAlaIleThrIleSerCysGlnValAsnLysSerAspAspSerValIleGlnLeuLeuAsn 76
QY 121 CCCAACAGGACAGCATTTACTTCAGGAGCTTCAGGCTTTGAAGAGACAGCAGGTTTCAG 180
Db 77 ProAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 96
QY 181 CTTGCGAATTTTCTTACGACGACCAAGTCTACCTGACCAATCTTCATCTCGGAT 240
Db 97 LeuLeuAsnPheSerSerSerIleuLysValSerLeuThrAsnValSerIleSerAsp 116
QY 241 GAAGGAGATTAATCTTCAGAGCTTACAGGAGACCCCAAGAGAGATTAACACACATC 300
Db 117 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 136
QY 301 ACAGTCCTGCTTCCTCCACGTAAGTTCGATGATGATATCCAGAAACACAGCGAGTTGAA 360
Db 137 ThrValIleValIleProProArgAsnLeuMetIleAspIleGlnLysPheThrAlaValGlu 156
QY 361 GGGGAGGAGATTCAGATGACGTAAGTCTGACGAGCCAGACCCAGGAGGAGCATCAGG 420
Db 157 GlyGluGluIleGluValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg 176

QY 421 TGGTTCAAGGAGCAAGCAAGCAACTCAAAAGCCAAATCAGAGCTGGAGAGTGTCGACATG 480
Db 177 TrpPheLysGlyAsnThrGluLeuLysGlyLysSerGluValGluIuThrPheSerAspMet 196
QY 481 TACACGTGTACCAAGTACGTAGTGCATGAGGTGCACACAGAGAGACAGCGGGTCCGGGTG 540
Db 197 TyrThrValIleThrSerGlnLeuMetLeuLysValHisLysGluAspAspIleValIleProVal 216
QY 541 ATCTGCCAGGTGAGAGACCCCTGGGTCACTGGGAACCTGCAGACCCAGCGATTCAGAA 600
Db 217 lIeCysGlnValGluHisProAlaValIleThrGlyAsnLeuGlnThrGlnArgTyrLeuGlu 236
QY 601 GTGCAGTATTAACCCGCAAGTGCATATCCAGATGACTTACCTCTGCAGAGCCCTAACCCGG 660
Db 237 ValGlnTyrLysProGlnValHisIleGlnMetTyrProLeuGlnGlyLeuThrArg 256
QY 661 GAAGGGGATGCATTTGAGTTAAAGCTGTGAAGCCATCGGAGAACCCCAAGCTGTGATGTA 720
Db 257 GlyGlyAspAlaLeuGluLeuThrCysGluAlaIleGlyLysProGlnProAlaMetVal 276
QY 721 ACTTGCGTGAAGTGCATGATGAATGCCCTCAACATGCCGTACTGTCGGCCAAACCTG 780
Db 277 ThrTrpValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
QY 781 TTCATCAATTAACCTTAACAAACAGATTAACGGTACTTACCGCTGTGAGGCTTCACACATA 840
Db 297 PheIleAsnAsnLeuAsnLysThrAspAsnGlyTyrThrArgCysGlnLysAsnIle 316
QY 841 GTGGCAAGGCTCATTCGACATATATGCTGTATGATATACGATCCCCCAACATATCCCT 900
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QY 901 CCTCCCAACAACAGCAGCAGCACTACACACACACACACACACACATCCCTACCATCATC 960
Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleLeuThrIleIle 356
QY 961 ACAGATTCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1008
Db 357 ThrAspSerArgAlaGlycIuGlySerIleArgAlaValAspHis 372

RESULT 7
US-09-944-449-61
; Sequence 61, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botsstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997

;; PRIOR APPLICATION NUMBER: 60/069335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440

;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-449-61
Alignment Scores:
Pred. No.: 6,11e-114
Score: 1741.00
Percent Similarity: 99.11%
Best Local Similarity: 98.81%
Query Match: 96.51%
DB: 10
Length: 440
Matches: 332
Conservative: 1
Mismatches: 3
Indels: 0
Gaps: 0
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QY 121 CCCAAGAGGACGACCATTTACTTCAGGACTTCAGGCTTTGAAGGACAGCAGTTTCA 180
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Db 77 Proasnarglnthrlleryrphearqasppheargproleuylsaspserrargphegl 96
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QY 181 CTGCTGAATTTTCTAGCAGTGAACCTCAAGTGTCACTGCAATGCTTCATCTCGAT 240
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QY 241 GAAGGAGATATCTTGTGCCAGCTCTACAGGACCCCCACAGAGAGATTACACCACAT 300
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QY 301 ACAGTCTGCTGCTCTCCAGCTACTGATGATGATGATGATGATGATGATGATGAT 360
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QY 361 GGGGAGAGATTTAGTCAACTGACTGATGCCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
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QY 781 TTCATCAATTAACCTTAACAACAAGATTAACGGTACTTACCGCTGAGGCTTCAACAT 840
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QY 841 GTGGGAAAGGCTCATCGGACGATATGCTGATGATGATGATGATGATGATGATGAT 900
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Db 117 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnIleSerTyrThrIle 136
QY 301 ACAGTCTGCTCCACGTAACCTGATGATATCCGAAGAAGCAGCGAGTTGAA 360
Db 137 ThrValLeuValProProAlaGlnLeuMetIleAspIleGlnIlySAspThrAlaValGlu 156
QY 361 GGGGAGGAGATTGAAGTCAACTGACTGCGCAGCAAGCCAGGAGGAGCAGCATCAGC 420
Db 157 GlyGlnIleGlnValAsnCysThrAlaMetAlaSerIlySProAlaThrThrIleArg 176
QY 421 TGGTTCAAGGAGCAAGCAACTCAAGGCAATCAGAGGTGGAGGAGGTGGCATG 480
Db 177 TrpPheIlySAlaThrThrGlnLeuIlySgIlySserGlnValGlnIlyTrpSerAspMet 196
QY 481 TACACTGTGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 540
Db 197 TyrThrValThrSerGlnLeuMetLeuValHisIlySgIlySAspArgIlyValProVal 216
QY 541 ATCTGCAAGTGGAGACCTGCGGTGCTGAGAAACCTGAGACCCAGCCTATCTAGAA 600
Db 217 IleCysGlnValGlnHisProAlaValThrGlyAsnLeuGlnThrGlnArgTyrLeuGln 236
QY 601 GTGAGATATAACCGCAAGTCAATCCAGATGACTTACCTCTGCAAGCCTTAACCCGG 660
Db 237 ValGlnTyrIlySProGlnValHisIleGlnMetThrTyrProLeuGlnIlyLeuThrArg 256
QY 661 GAAGGAGGATCATTTGAGTAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 257 GlnGlySAspAlaLeuGlnIleuThrCysGlnAlaIleGlnIlySProGlnProValMetVal 276
QY 721 ACTTGGTGAAGTGCATGATGAATGCAATCCCTCAACATGCCCTACTGTCTGGGCCAAACCTG 780
Db 277 ThrTyrValArgValAspAspGlnMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
QY 781 TTGATCAATATACCTAAACAAACAGATAGGTAACCGTCTGAGGCTTCCAAATA 840
Db 297 PheIleAsnIlySAsnLeuValThrAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 316
QY 841 GTGGGAAGGCTCATTCGACTATATGCTGATATGATATGATATGATATGATATGATATGATAT 900
Db 317 ValGlyIlySAlaHisSerAspTyrMetLeuTyrValTyrIlySProProThrThrIlePro 336
QY 901 CTCGCCCAACAAACACACACACTACCAACCAACCAACCAACCAACCAACCAACCAACCAAT 960
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QY 961 ACAGATCTGAGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1008
Db 357 ThrAspSerArgAlaGlyGlnGlnGlySerIleArgAlaValAspHis 372

RESULT 9
US-09-944-862-61
Sequence 61, Application US/09944862
Patent No. US2002015145A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gertlisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul
APPLICANT: Grumley, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US2002015145A1 December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US2002015145A1 December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000

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; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-862-61

Alignment Scores:
Pred. No.: 6,11e-114 Length: 440
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 10 Gaps: 0

US-09-778-187b-3_copy_62_1069 (1-1008) x US-09-944-862-61 (1-440)

QY 1 ATCCCAAGGTCGATGAGAGATCTTACTAAGACGTGACGTGATGAAGAGAA 60
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DB 57 VALATHTHLESERYSGINVALANLYSERASPSASERVALLEGINLEULASN 76
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DB 117 GLUGLYARGTYRHECYSGINLEUTYRTHASPROPROGLNLSERTYRTHRIIE 136
QY 301 ACAGCTCTGGTCTCTCCAGCTAACTTGATGATGATATCCAGAAGACAGGAGTTGAA 360
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QY 541 ATCTGCCAGGTGAGACACCTCGGCTACTGGAACCTGACAGCCAGCGCTATCTAGAA 600
DB 217 TLECYGLIVALTGLNHSIPROALVALTHRGLYASNLEUGLNTHRCINARGTYRLEUGLN 236
QY 601 GTGCAGTATTAACCGCAAGGATATCCAGATGACTTACCCCTGCAAGGCGCTAACCCGG 660
DB 237 VALGINTYRLYSERPROGLNVALHISILEGLNMETHTYRPROLEUGNLGYLEUTHARG 256
QY 661 GAAGGAGATGCAATTTGAGTTAACGTGTGAAGCCATCGGAAGCCCAAGCCTGTGATGTA 720
DB 257 GLUGLYASPRVALLEUGLNULEUTHRCYSGLVALALLEGLYLVSERPROGLNPROVALMETVAL 276
QY 721 ACTTGGGTGAGAGTCATGATGAATGCTCAACATGCGGTACTGTGGCCAAACCTG 780
DB 781 ACTTGGGTGAGAGTCATGATGAATGCTCAACATGCGGTACTGTGGCCAAACCTG 780
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DB 277 THTRPVALARGVALASPRGLUMETPROGLNHLASLAVALLEUSERGLYPROASNLEU 296
QY 781 TTCATCAATTAACCTAAACAACAGATTAACGTTACTTACCGTGTGAGCTTCAACATA 840
DB 297 PHLEIASNANLEUNSNLYSTRHASPANGLYTHRTYRARGYSGLVALASERANLIE 316
QY 841 GTGGGAAGGCTCATTCGACGTATATGCTGTATGATAGCATCCCCCAACACTATCCCT 900
DB 317 VALGLYSLALHISSEFASPTRYMETLEUTYRVALTYRASPROPROTHRIHLEPRO 336
QY 901 CCTCCCAACAACAACCAACCACTTACCAACCAACCAACCAACCACTTACCATCATC 960
DB 337 PROPROTHRTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 356
QY 961 ACAGATTCTCGACAGTGAAGAGGAGCATTGGGCACTGGAGCAC 1008
DB 357 THASPSERHARGALGLUGLUGLUGLYSERLIEARGALVALASPHLS 372

RESULT 10
US-09-945-587-61
; Sequence 61, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gertlson, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavio, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
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APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: 2001-09-26
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
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PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132768A1
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO: 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-945-015-61

Alignment Scores:
Pred. No.: 6,11e-114 Length: 440
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 10 Gaps: 0

US-09-778-187B-3_COPY_62_1069 (1-1008) x US-09-945-015-61 (1-440)

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DB 57 VALAIATHRLIISERCYGLNLSNLYSERSAPSPSERVALILEGLINLEUANA 76
QY 121 CCCAACGAGCAGACCATTAATTCTGAGGACTCAGGCTTGAAGAGCAGGTTTCAG 180
DB 77 PROASARGLHTRILLEYRPHENARGASPHEATGPROLEULYSSESRATGPHGLN 96
QY 181 CTGCTGAATTTTCTAGCAGTGAAGTCAAGTGTCACTGACGAATGTCAATCTCGAT 240
DB 97 LEULEASNPHERSERSESRERGLULEULYSVALSERLEUTHASVALSERLIESERAP 116
QY 241 GAAGGAGATTAATTCTGACGCTTACACGAGACCCCCACAGAGAGATTACACACCATC 300
DB 117 GLUGLYARGTYRPHECYGLNLEULYRTHRAAPPROGLINGLUSERYRTHRRILE 136
QY 301 ACAGTCCGTGTTCTCCACGTAATGATGATGATGATGATGATGATGATGATGATG 360
DB 137 THNVALLEUVALPROBROARGASNLEUKETILEASPILEGILYSPHRLAVALGLU 156
QY 361 GGGAGAGAGATTGAAGTCAACTGATGATGATGATGATGATGATGATGATGATGATG 420
DB 157 GLYGLUGLUIILEGLVALASNCYSTHRLALAMETALASERLYSPROBRLAHLRTHRIEARG 176
QY 421 TGGTTCAAAGGGAACAGGAACTCAAGGCAATCAAGAGTGGAGAGGTGTCGACATG 480
DB 177 TRPHLYGLYASNTHRSLIULEULYSGLYSSERGLUVALIGLUNTRPERASPMET 196
QY 481 TACACGTGACACGTCAGTGTGATGTCGAAGGTGCAACAGAGAGACAGGCGTCCCGGTG 540
DB 197 TYRTHVALTHRSERGLINLEUMETLEULYSVALIHSLYSGLIASPSPIYVALPROVAL 216
QY 541 ACTGTCAGAGTGAGACACCTCGGTCACTGGAACCTGACAGCCAGCGCTATGTAGAA 600
DB 217 IIECYSGINVALIGLUIHSIROALVALIHTRGLYASNLEUGLINTHCLINARGYRLIEUGLU 236
QY 601 GTGCAGTATTAACCCGACAGTATTCAGATGACTTACCCTCTGCAAGGCTTAACCCGG 660

Db 237 ValGlnIyrIysProGlnValHisIleGlnMetThrIyrProLeuGlnGlyLeuThrArg 256
QY 661 GAAGGGATCATTTGATTAACGTGTGAAGCCATCGGAAGCCCGGCTGTGATGGTA 720
Db 257 GlnGlyAspAlaLeuGlnGlnLeuThrCysGlnAlaIleGlyIysProGlnProValMetVal 276
QY 721 ACTTGGGTGAGCTCGATGATGAATGCCCAACATGCCCTACTGTCTGGCCCAACCTG 780
Db 277 ThrTrpValArgValAspAspGlnMetProGlnHisAlaValLeuSerGlyProAsnLeu 296
QY 781 TTGATCAATACCTAAACAAACAGATTAACGGTACTTACCGCTGTGAGGCTTCCACATA 840
Db 297 PheIleAsnIleuAsnIleuSlnIyrThrAspAsnGlyThrIyrArgCysGlnAlaSerAsnIle 316
QY 841 GTGGAAAGGCTCATTCGGCTATATGCTGTATGATATACATGCCCGCCACACTATCCCT 900
Db 317 ValGlyIysAlaHisIleSerAspIyrMetLeuIyrValIyrAspProIyrThrIlePro 336
QY 901 CCTCCCAACAACACACACACACTACACACACACACACACACATCCTTACCATCATC 960
Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIlePro 356
QY 961 ACAGATTCCTGACAGCTGAAGGGGACCATTCGGGCGACTGCACAC 1008
Db 357 ThrAspSerArgAlaGlyIleGlnGlySerIleArgAlaValAspHis 372

RESULT 12

US-09-944-396-61

Sequence 61. Application US/09944396

Patent No. US20020132981A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Baton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerdtzen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kljavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944,396

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-396-61

Alignment Scores:
Pred. No.: 6,11e-114 Length: 440
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 10 Gaps: 0

US-09-778-187B-3_copy_62_1069 (1-1008) x US-09-944-396-61 (1-440)

PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 23, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020142419A1 September 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020142419A1 September 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-432-61
Alignment Scores:
Pred. No.: 6,11e-114 Length: 440
Score: 1741.00 Matches: 332

Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 10 Gaps: 0
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QY 121 CCCAAGCGACAGACATTTACTTCAGGACTTCAGGCTTTGAAGACAGACAGGTTTTCAG 180
Db 77 ProasnArgGlnThrLLeuPheThrLysAspPheArgProLeuLysAspSerArgPheGln 96
QY 181 CTGCTGAATTTTCTAGACGACTGAAGTCAAGTCAAGTCAAGTCTCAATCTCGGAT 240
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QY 241 GAAGGAGATACCTTCGCCGCTCTACCGACCCCCACAGAGATTACACCATC 300
Db 117 GlnGlyArgGlyPheCysGlnLeuTyrrThrAspProGlnLLeuSerTyrrThrLLe 136
QY 301 ACAGCTCGGTTCTCCACGCTAATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 137 ThrValLeuValProProAsnLeuMetLLeAspLLeGlnLysAspThrAlaValGlu 156
QY 361 GGGGAGAGATTGAAGTCAACTGTACTGCCATGGCCAGCAAGCCAGGACCATCAGG 420
Db 157 GlnGlnGlnLLeGlnValasnCysThrAlaMetAlaSerLysProAlaThrThrLLeArg 176
QY 421 TGCTTAAAGGAAAGCAAGGACGCTCAAGCAATCGAGGTGAGAGTGGTGAGCATG 480
Db 177 TrpPheLysGlnLsnThrGlnLeuLysGlnLysSerGlnValGlnLysTrpSerAspMet 196
QY 481 TACACTGTGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 197 TyrrThrValThrSerGlnLeuMetLLeuLysValHisLysGlnAspArgLysValProVal 216
QY 541 ATCTGCAGGTGAGACGACCTCGGCTGCTGTAAGTCAAGTCAAGTCAAGTCAAGTCA 600
Db 217 LLeCysGlnValGlnLsnProAlaValThrGlnLysLeuGlnThrGlnAlaGlyLLeuGln 236
QY 601 GTGCGATATTAACCGCAAGTCAATCCAGTACCTGACCTGCAAGGCTTAACCCGG 660
Db 237 ValGlnTyrrLysProGlnValHisLLeGlnMetThrTyrrProLeuGlnGlnLLeuThrArg 256
QY 661 GAAGGAGATGATTTGAGTTAAAGTGTGAAGCATCGGAAGGCCAGCTGTGATGATGTA 720
Db 257 GlnGlnLysAspAlaLeuGlnLLeuThrCysGlnAlaLLeLLeLysProGlnProValMetVal 276
QY 721 ACTTGGGTGAGAGTCGATGATGAATGCCATCAACATGCCCTACTGTGTGGCCAAACCTG 780
Db 277 ThrThrValArgValAspAspGlnMetProGlnHisLAlaValLeuSerGlyProAsnLeu 296
QY 781 TTTCATCAATTAACCTAAACAAACAGATTAAGGTAACCGCTGTGAGGCTTCCAACTA 840
Db 297 PheLLeasnAsnLeuAsnLysThrAspAsnGlyThrTyrrGlyGlnAlaLLeSerAsnLLe 316
QY 841 GTGGGAAAGGCTCATTCGAGCTATATGCTATGATATACATCCGCCCAACATATCCCT 900
Db 317 ValGlnLysAlaHisSerAspTyrrMetLeuTyrrValTyrrAspProProThrThrLLePro 336
QY 901 CTTGCCAACAACAACACACACTACACACACACACACACACACATCTTACCATCATC 960
Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrLLeuThrLLe 356
QY 961 ACAGATTCTCGACGATGAGAGGAGGACATTTGGGCACTTGACACAC 1008

Db 357 ThrspserArgAlaGlyGluGlySerIleArgAlaValAspHis 372
RESULT 15
US-09-943-762-61
Sequence 61, Application US/09943762
Patent No. US20020142958A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bolstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/943,762
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517

;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020142958A1member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020142958A1member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-943-762-61

Alignment Scores:
Pred. No.: 6,11e-114 Length: 440
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: Gaps: 0

US-09-778-187b-3_copy_62_1069 (1-1008) x US-09-943-762-61 (1-440)
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QY 37 ILeProThrcIyAspGlyInAsnLeuPheThrIyAspValThrValIleGluGlyIlu 56
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GTGGCAACCATCGTCGCCAGTCATTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 57 ValAlaThrIleSerCysGlnValAlaSnIySerAspAspSerValIleGlnIleuLeuAsn 76
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 CCCACAGCAGACACATTACTTCAGGACCTTCAGGCTTTGGAAGACAGAGTTTCAG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 77 ProAsnArgGlnThrIleIyrrPheAsnArgPheAsnArgProIleuIyAspSerArgPheGln 96
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 CTGCGTAATTTTCTAGCAGTGAATCAAGTGTCTCAGTGAAGTGTCAATTCGGAT 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 97 LeuLeuAsnPheserSerSerGlnLeuIyValSerLeuThrAsnValSerIleSerAsp 116
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QY 241 GAAGGAGATCTTCTGCCAGCTCTACAGGACCCGCCACAGAGAGTTCACACCATC 300
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QY 117 GluGlyArgTyPheCysGlnLeuTyrrThrAspProGlnGluSerTyrrThrIle 136
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QY 137 ThrValLeuValProProIyAsnLeuMetIleAspIleGlnIlyAspThrAlaValGlu 156
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QY 361 GGGGAGGAGATTGAAGTCAACTGTACTGCCAATGCCACGACGACGACGACATCAG 420

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Db 157 G|YGLuG|L|I|eG|L|uV|a|I|n|c|y|s|t|H|a|L|a|S|e|r|L|y|S|P|o|a|I|a|T|H|I|L|e|a|g 176
OY 421 TGGTTCAAGGGGAACAAAGCAACTCAAAAGCAAAATCAGAGGTGGAGGATGTCGACATG 480
Db 177 TTPPh|e|L|y|S|G|I|y|a|n|H|r|g|L|u|e|u|L|y|S|G|I|y|L|y|S|e|r|G|I|u|a|I|G|I|u|I|n|T|P|S|e|r|a|S|P|e|t 196
OY 481 TACACTGTGACCACTGACGTGATGCTGAAGGTGCACACAGAGGACGACGAGGTCCCGTG 540
Db 197 T|y|T|H|V|a|I|T|H|S|e|r|I|n|L|e|u|M|e|L|u|S|V|a|I|H|I|S|L|y|S|G|I|u|S|P|a|S|P|G|I|y|V|a|I|P|r|o|V|a|I 216
OY 541 ATCTGCCAGGTGGAGACCCCTGCGGTCACTGGCAAACTGCAGACCCAGCGCTATCTAGAA 600
Db 217 I|L|e|C|y|S|G|I|n|V|a|I|G|I|u|H|I|S|P|r|o|I|a|V|a|I|T|H|G|I|y|a|S|n|L|e|u|G|I|n|T|H|G|I|n|a|g|T|y|L|e|u|G|I|u 236
OY 601 GTGCATATTAACCGCAAGCGCATATCCAGATCACTTACCCTTGCAGGCGCTAACCCGG 660
Db 237 V|a|I|G|I|n|T|L|y|S|P|r|o|I|n|V|a|I|H|I|S|I|L|e|G|I|n|M|e|T|H|T|y|P|r|o|L|e|u|G|I|n|G|I|y|L|e|u|H|a|g 256
OY 661 GAAGCGCATGCATTTGAGTTAACTGTGAAGCCATCGGAAAGCCCGCAGCCTGTGATGTA 720
Db 257 G|L|u|G|I|y|a|S|P|a|I|L|e|u|G|I|u|e|u|H|r|c|y|S|G|I|u|a|I|a|I|L|e|G|I|y|S|P|r|o|I|n|P|r|o|V|a|I|L|e|t|V|a|I 276
OY 721 ACTTGGGTGAGAGTCGATGATGAATGCTCAACATGCGGTACTGTGTGGCCAAACTG 780
Db 277 T|H|T|P|V|a|I|a|g|V|a|I|a|S|P|a|S|P|G|I|u|e|L|P|r|o|I|n|H|I|S|A|I|a|V|a|I|L|e|u|S|e|r|G|I|y|P|r|o|a|S|n|L|e|u 296
OY 781 TTCATCAATTAACCTTAACAAACAGATTAACGGTACTTACCGCTGTGAGCCTTCCACATA 840
Db 297 P|H|e|I|L|e|a|S|n|S|n|L|e|u|S|n|L|y|S|T|H|P|a|S|P|a|S|n|G|I|T|H|T|y|a|g|C|y|S|G|I|u|a|I|a|S|e|r|a|S|n|I|L|e 316
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OY 901 CCTCCACAACAACGACACCACTACACGACGACCAACACCACTCCTTACCATCATC 960
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OY 961 ACAGATTTCGAGAGTGAAAGGAGGACCATTTGGGGAGTGAGACCAAC 1008
Db 357 T|H|a|S|P|S|e|r|a|g|a|I|a|G|I|y|G|I|u|G|I|y|S|e|r|I|L|e|a|g|a|I|a|V|a|I|a|S|P|H|I|S 372
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Search completed: November 20, 2002, 08:17:28
Job time : 21 secs

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SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	1765	97.8	423	21	AAV45093	Mouse lymphoid derived dendritic cell adhesion molecule.
2	1741	96.5	402	22	AAM23691	Human EST encoded
3	1741	96.5	440	20	AAV17830	Human PRO355 prote
4	1741	96.5	440	21	AAB01321	Human PRO355 polyp
5	1741	96.5	440	22	AAU29040	Human PRO polypept
6	1741	96.5	442	21	AAB25619	Protein encoded by
7	1741	96.5	442	21	AAV94341	Human cell surfac
8	1741	96.5	442	21	AAV45092	Human lymphoid de
9	1741	96.5	442	23	AAE19887	Human tumour supp
10	1694	93.9	364	21	AAB25586	Protein encoded by
11	1592.5	88.3	443	22	AAB88427	Human membrane or
12	1571	87.1	414	21	AAV53028	Human secreted pte
13	1133.5	62.8	229	21	AAB25593	Protein encoded by
14	631	35.0	387	22	AAW78418	Human protein SEQ
15	625.5	34.7	444	20	AAV33741	Beta-secretase. H
16	625.5	34.7	444	22	ABA47251	Beta-secretase. H
17	606	33.6	388	22	ABB11897	Human F2162_1 hom
18	599	33.2	388	22	AAW79402	Human protein SEQ
19	580.5	32.2	404	23	ABG66677	Human novel polype
20	578.5	32.1	404	22	AAAB61142	Human NOV12 prote
21	480.5	26.6	398	21	AAE69287	Amino acid sequen
22	480.5	26.6	404	22	AAE00868	Mouse brain immunc
23	472.5	26.2	564	21	AAV94406	Human ACAM4/Tg4-F-E
24	471.5	26.1	368	21	AAV94405	Human ACAM4/Tg4-F-
25	470.5	26.1	598	21	AAV94404	Human ACAM6/Tg4-F-
26	469.5	26.0	398	19	AAH80405	A secreted protein
27	469.5	26.0	398	20	AAV29592	Human MBGP1 prote
28	469.5	26.0	398	20	AAV13358	Amino acid sequen
29	469.5	26.0	398	21	AAV94403	Human ACAM cellulid
30	469.5	26.0	398	21	AAV69288	Amino acid sequen
31	469.5	26.0	398	21	AAV45095	Human LDCAM bindin
32	469.5	26.0	398	22	AAU12245	Human PRO258 polyp
33	469.5	26.0	398	22	AAAB80226	Human PRO258 prote
34	469.5	26.0	398	22	AAB53083	Human anglogenesisI
35	469.5	26.0	398	23	ABP61823	Human polypeptide
36	469.5	26.0	398	23	ABB95444	Human angiogenesisI
37	469.5	26.0	398	23	ABBB4838	Human PRO258 prote
38	469.5	26.0	413	22	AAE00867	Human brain immunc
39	467.5	25.9	344	22	ABBS1281	Human secreted pte
40	467.5	25.9	367	22	ABBS1280	Human secreted pte
41	467.5	25.9	432	21	AAV94402	Human ACAM cellulid
42	467.5	25.9	432	21	AAV69286	Amino acid sequen
43	467.5	25.9	432	21	AAV45094	Human LDCAM bindin
44	467.5	25.9	432	22	ABBS0413	Human secreted pte
45	457	25.3	433	21	AAV53472	Human Beat-like I
ALIGNMENTS						
RESULT 1						
AAV45093						
ID	AAV45093	standard; Protein; 423 AA.				
XX	AAV45093;					
AC						
DT	31-MAY-2000	(first entry)				
DE	Mouse lymphoid derived dendritic cell adhesion molecule.					
XX						
KM	Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1;					
KW	B7-L1; T cell proliferation; natural killer cell; NK; tumour cell;					
RN	biological activity; quality control reagent; inflammation;					
KX	immune system disorder; autoimmune; viral infection; infectious disease;					
XX	organ transplant rejection; bone marrow; modulator; immune response.					
OS	Mus sp.					
PH	Key	Location/Qualifiers				

FT Domain 1..356
 FT /label= Extracellular_domain
 FT Modified-site 49..51
 FT /note= "N-glycosylation site"
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 FT /note= "N-glycosylation site"
 FT Modified-site 95..97
 FT /note= "N-glycosylation site"
 FT Modified-site 147..149
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 FT Modified-site 286..288
 FT /note= "N-glycosylation site"
 FT Modified-site 290..292
 FT /note= "N-glycosylation site"
 FT Domain 357..377
 FT /label= Transmembrane_domain
 FT Domain 378..423
 FT /label= Cytoplasmic_domain
 PN WO200008158-A2.
 PD 17-FEB-2000.
 XX
 XX 05-AUG-1999; 99WO-US17905.
 PR 07-AUG-1998; 98US-0095672.
 XX
 XX (IMV) IMMUNEX CORP.
 PI Baum PR, Fanslow WC;
 XX
 DR WPI: 2000-205712/18.
 DR N-PSDB: AAZ50883.
 XX
 PT Novel molecules designated LDCAM are capable of altering or modulating
 PT T cell function

PS Claim 7; Page 46-47; 44pp; English.

CC The present amino acid sequence is the mouse lymphoid derived dendritic
 CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
 CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
 CC region of B7-1. Mouse LDCAM is found on whole embryo, testes, triple
 CC negative cells murine splenic and lymph node CD8+, S49.1 and dendritic
 CC cells. LDCAM polypeptides interacts with T cell surface molecules
 CC to alter signalling and inhibits T cell proliferation, bind to
 CC themselves and B7-1, an LDCAM binding protein and increases natural
 CC killer (NK) cell populations. It may be used to measure the biological
 CC activity and as quality control reagents of LDCAM binding proteins.
 CC LDCAM may be used for treating disorders associated with malfunctioning
 CC of immune system, inflammation, autoimmune disorders, viral infected
 CC cells, infectious diseases and for killing tumour cells. They are also
 CC useful for prevention or reducing the effect of organ and bone marrow
 CC transplant rejection and for modulating T cell immune responses. LDCAM
 CC polypeptides may also be used as carriers for delivering agents attached
 CC to T cells or cells bearing B7-1.

SQ Sequence 423 AA:

Alignment Scores:
 Pred. No.: 2,03e-148 Length: 423
 Score: 1765.00 Matches: 336
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.84% Indels: 0
 DB: 21 Gaps: 0

US-09-778-187b-3_COPY_62_1069 (1-1008) x AAY45093 (1-423)

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OY 61 GTGGCAACCATCAGCTGCCAGGTCAATTAAGATGAGACTCACTGATCCAGCTCTGAAAC 120
 DB |||||
 OY 41 VALAIAATHRIIESERCYSGINVALASNLYSSERASPSPSERVALIIEGLINLEUENAS 60
 DB |||||
 OY 121 CCCAACAGGAGAGCCATTACTTCAGGAGCTTCAGGCTTTGAAGACAGACAGATTTCAG 180
 DB |||||
 OY 61 PROASNARGLINHRIILEYRPHENARGSPHENARGPROLEUYSASPSPSERARGPHEGIN 80
 OY 181 CTGCTGAATTTTCTGACATGACATCAAAAGTGCATGCGAATGTCATCTCGAT 240
 DB |||||
 OY 81 LEULEASNPHESERSESRERGLULEULYSVALSERLEUTHRSNVALSERLIESEARSP 100
 OY 241 GAAGGAGATATCTTCCAGCTCTACACGACGCCCCACAGGAGATTACACCAACATC 300
 DB |||||
 OY 101 GLUGLYARGTYRPHECYSGINLEUTYRTHASPPROGLINLSERTYRTHRIIE 120
 OY 301 ACAGTCTGCTTCTCCAGCTAACTTGATGATGATATCCAGAAACACAGCGATTTGAA 360
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 OY 121 THRVALLIENVALPROPROARGASNLEUMELLEASPIIEGLINYSASPTRHAIALAIGLI 140
 OY 361 GGGGAGAGATTGAGTCAACTGACTACTGATGCCATGCGCAGCAGCAGCAGCAGCAGCAG 420
 DB |||||
 OY 141 GLYGLUGIULEGLIENVALASNCYSTRHAIAMETALSERLYSPROALATHRIIEARG 160
 OY 421 TGCTTCAAGGAGAACAGCAAGCAACTCAAGGCAATTCAGAGTGGAGAGTGTGCACATG 480
 DB |||||
 OY 161 TRPPELHLYSGLYASNLYSGINLEULYSGLYLYSSEGLIVALIGIUIRTPSERASPMEI 180
 OY 481 TACACTGTGACCGATGATGATGCTGGAAGGTGCACAAAGAGAGACAGCGGGTCCGGTG 540
 DB |||||
 OY 181 TYRTHRVALLIHTSERGLINLEUMELLEULYSVALHISLYSEGLIUSPASPGLYVALI 200
 OY 541 ATCTGCAGGTGGAGCACCCTGGCTGCTGCAAGACCTGACAGCCAGCGCTATAGAA 600
 DB |||||
 OY 201 IIECYSGINVALGINHISPROALAVAITHNGLYASNLEUGINHTRGLINARGTYRLEUGLI 220
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 OY 661 GAAGGAGATGCAATTAGATTAAAGTGTGAAGCCATGCGGAGGCCAGCTGTGATGGTA 720
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 OY 241 GLUGLYASPLAHEGLIENLEUTHRCYSGIUALAIEGLYLYSPROGLINPROVALIMETVAL 260
 OY 721 ACTTGGGTGAGAGTCCATGATGATGAATGCTCAACATGCGCTGCTGGGCGCAACCTG 780
 DB |||||
 OY 261 THRTPRVALARGVALASPSRGLIUMETPROGLINHISALVALLEUSERGLYPROASNLEU 280
 OY 781 TTCATCAATPACCTAAACAACAGATAACGGTACTTACCGCTGTGAGCGTTCACACATA 840
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 OY 281 PHEILEASNASNLEUASNLYSTRASPASNGLYTHRYARGCYSGIUALASERASNILE 300
 OY 841 GGGGAAAGGTCATTCGCGACATATATGCTGATGCTGTATGATGCCCGCAACTATCCGT 900
 DB |||||
 OY 301 VALGILYVALAHISSESRSPYRMELEUTYRVALTYASPPROTHRIIELEPTRO 320
 OY 901 CCTCCCAACAACAACACACACATACACACACACACACACACACACACATCTTACATCATC 960
 DB |||||
 OY 321 PROPTHTHRTHTHRTHTHRTHTHRTHTHRTHTHRTHTHRTHTHRTHTHRTHTHRIIELE 340
 OY 961 ACAGATTCTGACAGCAGTGAAGAGGGGACCATTTGGGCGAGTGAGACAC 1008
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 OY 341 THRASPSEARGLAIGLYGLUGIUGIYTHRIIEGLYALVALASPHTS 356
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 DB AAM23691
 DB ID AAM23691 standard; Protein; 402 AA.
 DB AC AAM23691;
 DB XX
 DB XX 12-OCT-2001 (first entry)
 DB XX Human EST encoded protein SEQ ID NO: 1216.

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XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KM diagnostics; forensic test; gene mapping; genetic disorder;
KM biodiversity; gene therapy; nutrition.
XX Homo sapiens.
XX MO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX PA
XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundl V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI: 2001-476164/51.
XX DR N-PSDB; AAH98350.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX PS
XX Claim 20: Page 877-878; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a
XX CC protein of the invention.
XX SQ Sequence 402 AA:
Alignment Scores:
Pred. No.: 2,72e-146 Length: 402
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 22 Gaps: 0
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OY 1 ATCCCCACAGCTGATGAGACAGATCTGTTTAAAGACGTGACAGTGTAGAGAGAA 60
DB 39 IIEPOTHGILYASPGILYASINLEUPHETHTLYASPAVALTHRVALLIEGLUGILGU 58
OY 61 GTGGCAACCATGAGTCCGAGGTCAATAGAGTACGAGTCACTGATCCAGCTCCGAC 120
DB 59 VALAATHILISERCYSGLNVALSNLYSSEASPSPSERVALLEGLNLEUENASN 78
OY 121 CCCAAGCAGCAGACCATTTACTTCCAGGACCTTCAGGCTTTGAGGACGAGGTTTCAG 180
DB 79 PROANARGGINTHTLLETYRHEARGASPHETARGPROLEULYASPSERTARGHGIN 98
OY 181 CTGCTGAAATTTTCTAGCAGTCACTCAAGTGTCACGTGACGAATGCTCAATCTCGGAT 240
DB 99 LEULENASNPHESERSESERGLNLEULYSVALISERLEUTHRASNVALISERTILESERASP 118
OY 241 GAAGGAGATCTTGTCCAGCTTACACGAGACCCGCCACGAGAGAGATCAACACCATC 300
DB 119 GUGLYARGTYRPHECYSGLNLEUTYRTHRASPPTROGILNGLISERTYRTHRTHTLIE 138
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OY 301 ACAGTCTGCTGCTCTCCACGTAACCTTGATGATGCATATCCAGAAAGACAGCGACTGAA 360
DB 139 THRVALLLEUVALPROBARGASINLEUMETILEASPDILEGLINYSAPTHRALAVALIGLU 158
OY 361 GGGGAGGACATGAACTGACACTGTACTGGCATGGCCAGACGACGACGACGACCATCAG 420
DB 159 GILGILGILNILEGLVALSNLCYSTNRALAMECALISERTYSPROALATHRTHTLIEARG 178
OY 421 TGGTTCAAGGAGAACAGAGACTCAAGGCAAAATCAGAGGTGGAGGAGTGTCGACATG 480
DB 179 TRPHELYSGLYASNTHRLLEULYSGLYLSSERGLVALIGLUILURPSERAPMET 198
OY 481 TACACTGTGACCAAGTCAGTGTATGTAAGGTGCACAGAGAGACGAGCGGTCGCCGTG 540
DB 199 TYRTHRVALLTHRSERCLNLEUMETLEULYSVALINLSLYSGILNAPSPGLYVALPROVAL 218
OY 541 ATCTGCGACGTGAGACACCCCTGGCGTCACTGGAACCTTCAGAACCCAGCGGTATCAGAA 600
DB 219 ILCYSGILNVALIGLNIHISPRVALVALTHRGLYASNLEUGLNTHRGILNRYTRLEAGLU 238
OY 601 GTGACGATATAACCCGCAAGTCATATCCAGATGACTTACCCTCTGCAAGGCTTAACCCG 660
DB 239 VALGINTYRLYSPTROGLNVALINISTIEGLNMETHTYRPROLEUGLNGILYEURTHRARG 258
OY 661 GAAGGAGATGCATTTGAGTTAACTGTGAAGCCATCCGGAAGCCCGACGCTGATGATGTA 720
DB 259 GUGLYASPALALEUGLLEULYTHRCYSGILVALALEGLYLYSPROGLNPROVALMETVAL 278
OY 721 ACTGGGTGAGAGTGCATGATGAAATGCTCAACATGCGCGTACTGTCTGGCCAAACCTG 780
DB 279 THRTTRVALARGVALASPSAPGILMETPROGLNHSALVALLEUSERTLYLPROVALNLEU 298
OY 781 TTCATCATTAACCTTAACAAACAGATTAACGGTACTACCGCTGTAGGCTTCCACATATA 840
DB 299 PHEILEASNASNLEUASNLYSTHRASPAINGLYTHYRARGYSELNLAISERANILE 318
OY 841 GTGGGAAGCTCATTTGAGTATATGCTGTATGATGATACGATCCGCCCAACATATCCCT 900
DB 319 VALGILYALAHISSEASRPTYMETLEUTYVALTYLTYRASPPTROBTHRTHTLIEPRO 338
OY 901 CCTCCCAACAAACCCACCACTACACACACACACACCAACCAACCACTTCCATCCATC 960
DB 339 PROPTHRTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 358
OY 961 ACAGATTTCTGAGCAGCAGTGAAGAGGAGGACCATTTGGGACGTGAGCCAGC 1008
DB 359 THRASPSERTARGALAGLIGLUGLISERTILEARGALVALASPHLS 374
RESULT 3
AAV17830
ID AAV17830 standard; Protein; 440 AA.
AC AAV17830;
XX
XX 12-AUG-1999 (first entry)
XX
XX
XX Human PRO355 protein sequence.
XX
XX
XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
XX secreted protein; transmembrane protein; inflammation disorder.
XX
XX Homo sapiens.
XX
XX OS
XX PN MO9928462-A2.
XX PD 10-JUN-1999.
XX
XX PF 01-DEC-1998; 98WO-US25108.
XX
XX 25-FEB-1998; 98US-0075945.
XX 03-DEC-1997; 97US-0067411.
XX 11-DEC-1997; 97US-0069278.
XX 11-DEC-1997; 97US-0069334.
```

PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069694.
 PR 16-DEC-1997; 97US-0069696.
 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.

XX (GENTH) GENENTECH INC.

XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 PI Yuan J;

DR WPI: 1999-371118/31.
 DR N-PSDB; AAX80053.

XX Nucleic acids encoding PRO secreted and transmembrane proteins

PT Claim 12; Fig 27; 123pp; English.

CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.

XX Sequence 440 AA;

Alignment Scores:

Pred. No.: 2,8e-146 Length: 440
 Score: 1741.00 Matches: 332
 Percent Similarity: 99.11% Conservative: 1
 Best Local Similarity: 98.81% Mismatches: 3
 Query Match: 96.51% Indels: 0
 DB: 20 Gaps: 0

US-09-778-187b-3_COPY_62_1069 (1-1008) x AAY17830 (1-440)

QY 1 ATCCCCACAGGTGATGACAGATCTGTTACTAAAGACGTGACGATTGAGAGAA 60
 DB |||||||
 Db 37 ILEPRTHTGlyAspGlyGlnAsnLeuPheThrIlyAspValThrValIleGluGlu 56
 QY 61 GTGGCAACATCAGCTGCCAGGTCAATTAAGAGTACGACTCAGTATCCAGCTCTGAAC 120
 DB |||||||
 Db 57 VALAIAthIleSerCysGlnValAsnIlySerAspSerValIleGlnLeuAsn 76
 QY 121 CCCACAGCAGACCATTTACTTCTTCAAGGAGCTTCAAGGAGCAGGCTTTCAG 180
 DB |||||||
 Db 77 PROAsnAlGlnThrIleIlyPheArgAspPheArgProLeuIlySpsSerArgPheGln 96
 QY 181 CTGCTGAATTTTCTAGACGATCAAGTGTCTACTGACGATTCATCTCGAT 240
 DB |||||||
 Db 97 LeuLeuAsnPheSerSerSerGlnLeuIlyValSerIleThrAsnValSerIleSerAsp 116
 QY 241 GAAGGAGATTTCTTCCAGCTCTACACGACCCCCACAGAGAGAGTACACCCACATC 300
 DB |||||||
 Db 117 GluGlyArgIlyPheCysGlnLeuIlyThrAspProGlnGlnIlySerIlyThrThrIle 136
 QY 301 ACAGTCCTGTTCTCCACGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB |||||||
 Db 137 ThrValIleValProProArgAsnLeuMetIleAspIleGlnIlySpsThrIleValGlu 156
 QY 361 GGGGAGGAGATTGAAGTCAATGCTATGCGATGCCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
 DB |||||||
 Db 157 GlyGluGluIleGlnValAsnIlyThrIleMetIleSerIlyProAlaThrThrIleArg 176

QY 421 TGGTTCAAAGGAACAAGAACTCAAAAGCAATTCAGAGGTGAGAGTGTGACATG 480
 DB |||||||
 Db 177 TrpPheIySgIlyAsnThrIleuIlySgIlySerClnValIleGluIlyTrpSerAspMet 196
 QY 481 TACACTGTGACAGTACGCTGATGCTGAAAGTGCACAGAGAGAGAGAGGAGGCTCCGGT 540
 DB |||||||
 Db 197 TyrThrValThrSerGlnLeuMetIlyValIleIlySgIlySpsArgIlyValProVal 216
 QY 541 ATCTGCCAGGTGAGACACCCGCGGTGATGAGAACTGAGACCCAGCCCTTTCAGAA 600
 DB |||||||
 Db 217 IleCysGlnValIleGlnIlySpsProAlaValThrGlyAsnLeuIlyThrGlnArgIlyGlu 236
 QY 601 GTGCAGATTAACCCGCAAGTGCATATCCAGATGACTTACCCCTGCAAGGCTTAACCCG 660
 DB |||||||
 Db 237 ValGlnIlyTrpSproGlnValIleIleGlnMetThrTyProLeuGlnIlyLeuThrArg 256
 QY 661 GAAGGGATGCTATTGATTAACGTGTGAAGCCATGCGGAGAGCCCAAGCTGTGATGTA 720
 DB |||||||
 Db 257 GluGlyAspAlaLeuGlnLeuThrCysGlnAlaIleGlyIlySproGlnProValMetVal 276
 QY 721 ACTGGGTGAGAGTCGATGTAATGCGTCAACATGCGGTACTGTCTGGGCGCAACCTG 780
 DB |||||||
 Db 277 ThrTrpAlaArgValAspAspGlnMetProGlnIleIleValIleuSerGlyProAsnLeu 296
 QY 781 TTCATCAATTAACCTTAACAACAAGATTAACGTTACTTACCGCTGTGAGGCTTCCACATA 840
 DB |||||||
 Db 297 PheIleAsnAsnLeuAsnIlyThrAspAsnGlyThrTyArgIlySgIlyAlaSerAsnIle 316
 QY 841 GTGGGAAAGGCTATTCGGACTATATGCTGTATGTTATGATATCCCCACACTATCCCT 900
 DB |||||||
 Db 317 ValGlyIlySgIlyAlaIleSerAspIlyMetLeuTyValIlyTrpProThrThrIlePro 336
 QY 901 CCTCCCAACAACACACACACATACACACACACACACACACACACACATTCCTTACATCATC 960
 DB |||||||
 Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 356
 QY 961 ACAGATTCTGAGCAGAGTGAAGAGGAGACCATTTGGGAGGTGAGACAC 1008
 DB |||||||
 Db 357 ThrAspSerArgIleGlyGlnIlySerIleArgAlaValAspHis 372

RESULT 4
 AAB01321
 ID AAB01321 standard; Protein; 440 AA.
 AC AAB01321;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Human PRO355 polypeptide.
 XX
 KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;
 KW PRO343; PRO715; PRO241; PRO293; PRO323; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT
 FT Modified-site
 FT /label= Signal peptide
 FT 9..15
 FT /note= "N-myristoylation site"
 FT 65..69
 FT /note= "N-glycosylation site"
 FT 99..103
 FT /note= "N-glycosylation site"
 FT 111..115
 FT /note= "N-glycosylation site"
 FT 163..167
 FT /note= "N-glycosylation site"
 FT 227..233
 FT /note= "N-myristoylation site"
 FT 233..240
 FT Modified-site

FT Modified-site /note="Tyrosine kinase phosphorylation site"
FT 302...306
FT /note="N-glycosylation site"
FT 306...310
FT Modified-site /note="N-glycosylation site"
FT 307...313
FT Modified-site /note="N-myristoylation site"
FT 319...328
FT Modified-site /note="Tyrosine kinase phosphorylation site"
FT 365...371
FT /note="N-myristoylation site"
FT 372...393
FT Domain /label=Transmembrane domain
FT 376...382
FT Modified-site /note="N-myristoylation site"
FT 402...408
FT Modified-site /note="N-myristoylation site"
FT 411...417
FT Modified-site /note="N-myristoylation site"
FT 427...433
FT Modified-site /note="N-myristoylation site"
FT 428...432
FT Modified-site /note="N-myristoylation site"
FT 430...434
FT Modified-site /note="N-glycosylation site"
FT /note="N-glycosylation site"
PN WO20032776-A2.
XX 08-JUN-2000.
XX 01-DEC-1999: 99WO-US28301.
XX 01-DEC-1998: 98WO-US25108.
PR 16-DEC-1998: 98US-0112850.
PR 22-DEC-1998: 98US-0113296.
XX (GETH) GEMENTECH INC.
PA Baker KP, Botstein D, Eaton DL, Ferrara N, Fliviaroff E;
PI Gerlstein ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kijavlin IU, Napier MA, Roy MA, Tumas D, Wood WI;
XX WPI: 2000-412324/35.
DR N-PSDB: AAA49563.
XX
XX New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
XX Claim 12: Fig 24: 187pp: English.
XX
XX New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources.
XX
SQ Sequence 440 AA:
Alignment Scores:
Pred. No.: 2.8e-146 Length: 440
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 21 Gaps: 0
US-09-778-187b-3_COPY_62_1069 (1-1008) x AAB01321 (1-440)
QY 1 ATCCCCAGAGTGATGGACGAAATCTGTTTAAAGACGTGACACTGATTGAGAGAGAA 60
QY

|||||
Db 37 lIePrOthrGlyAspELyGlnAsnLeuPheThrLySAspValThrValIleGluGlu 56
QY 61 GTGGCAACCATYAGCTGCGAGGTCAATAAGAGTGCAGACTGATGCCAGCTCCGAAAC 120
Db 57 ValAlaThrIleSerCysInValAsnLySAspAspSerValIleGlnLeuLeuAsn 76
QY 121 CCCAACAGGCACACATTTACTTCAGGGACTTCAGCCCTTTGAAGACAGAGCTTCAAG 180
Db 77 ProAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLySAspSerArgPheGln 96
QY 181 CTGCTGAATTTTCTAGCAGTGAACCTCAAGGTCACTGACCAATCTCATCTCCGAGT 240
Db 97 LeuLeuAsnPheserSerSerGlnLeuLySValSerLeuThrAsnValSerIleSerAsp 116
QY 241 GAAGGAGATACTTCTGCGAGCTTACAGAGACCCCGCCAGAGAGATTACACCAACATC 300
Db 117 GluGlyArgTyrPheCysInLeuTyrThrAspProGlnGlnSerTyrThrIle 136
QY 301 ACAGTCTGCTTCCTCCACGTAACTTGATGATGATATCCAGAAAGACAGCGCAGTTGAA 360
Db 137 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLySAspThrAlaValGlu 156
QY 361 GGGGAGAGATTTGAAGTCACTGTACTGCCATTCGCCAGAACCCAGCAGCAATCAGG 420
Db 157 GlyGluGluIleGlnValAsnCySThrAlaMetAlaSerLySProAlaThrThrIleArg 176
QY 421 TGGTTCAAGGAGAACAGGACCAAGGCAAAATCAGAGGTGAGAGAGTGCAGCATG 480
Db 177 TrpPheLySGlyAsnThrIleuLeuLySGlyLySserGlnValGlnIleThrPheSerAspMet 196
QY 481 TACACTGTGACCAAGTCAGCTGATGCTGAAGGTGCACAGAGAGACAGCGGCTCCGGTG 540
Db 197 TyrThrValThrSerGlnLeuMetLeuLySValIleLySGlnAspAspIleValProVal 216
QY 541 ATCTGCCAGGTGGAGACCCCTGGGCTCACTGGAACCTGCAGACCCAGCGCTATCTAGAA 600
Db 217 IleCysGlnValGlnIleAspProAlaValIleThrGlyAsnLeuGlnIleThrIleGlyLeuGlu 236
QY 601 GTGCAGTATTAACCGGCAAGTGCATATCCAGATGACTTACCTCTGCAAGGCCATACCCGG 660
Db 237 ValGlnTyrLySProGlnValIleIleGlnMetThrTyrProLeuGlnIleuThrIleArg 256
QY 661 GAAGGGATGCATTTGAGTTAAGCTGTGAAGCCATCGGAAAGCCCGAGCTGTGATGTA 720
Db 257 GluGlyAspAlaLeuGlnIleuThrCysGlnAlaIleGlyLySProGlnProValMetVal 276
QY 721 ACTTGGGTGAGAGTGCATGATGAATGCCCTCAACATGCCGTACTGTCTGGGCCAAACCTG 780
Db 277 ThrTrpValArgValAspAspGlnMetProGlnIleAlaValIleuSerGlyProAsnLeu 296
QY 781 TTTCATCAATTAACCTTAACAAACAGATTAACGGTACTTACCGCTGTAGGCTTCCACATA 840
Db 297 PheIleAsnAsnLeuAsnLySThrAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 316
QY 841 GTGGGAAGGCTCATTCGGACTATATGCTGTATGTATAGATGCCCGCCCAACATATCCCT 900
Db 317 ValGlyLyAlaIleHisSerAspTyrMetLeuTyrValTyrAspProProThrThrIlePro 336
QY 901 CCTCCCAACAACAACCCACACACTACCACACACACACACACACACATCTCTTACCATATC 960
Db 337 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIle 356
QY 961 ACAGATTCTCGAGCAGGTGAAGAGGAGGACCATTTGGGAGTGGAGACAC 1008
Db 357 ThrAspSerArgAlaGlyGluGlnGlySerIleArgAlaValAspHis 372
RESULT 5
AAU29040 standard: Protein; 440 AA.
ID AAU29040
AC AAU29040;
XX

DT	18-DEC-2001	(first entry)
XX		
DE	Human PRO polypeptide sequence #17.	
XX		
KW	PRO polypeptide: mammal; tumour; cancer; human; cattle; horse; sheep;	
KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;	
KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;	
KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200168848-A2.	
XX		
PD	20-SEP-2001.	
XX		
PF	28-FEB-2001; 2001WO-US065520.	
XX		
PR	01-MAR-2000; 2000WO-US05601.	
PR	02-MAR-2000; 2000WO-US05841.	
PR	03-MAR-2000; 2000US-187202P.	
PR	06-MAR-2000; 2000US-186968P.	
PR	14-MAR-2000; 2000US-189320P.	
PR	14-MAR-2000; 2000US-189328P.	
PR	15-MAR-2000; 2000WO-US06884.	
PR	21-MAR-2000; 2000US-190828P.	
PR	21-MAR-2000; 2000US-191007P.	
PR	21-MAR-2000; 2000US-191048P.	
PR	21-MAR-2000; 2000US-191314P.	
PR	28-MAR-2000; 2000US-192655P.	
PR	29-MAR-2000; 2000US-193032P.	
PR	29-MAR-2000; 2000US-193053P.	
PR	30-MAR-2000; 2000WO-US08439.	
PR	04-APR-2000; 2000US-194449P.	
PR	04-APR-2000; 2000US-194647P.	
PR	11-APR-2000; 2000US-195975P.	
PR	11-APR-2000; 2000US-196000P.	
PR	11-APR-2000; 2000US-196187P.	
PR	11-APR-2000; 2000US-196690P.	
PR	11-APR-2000; 2000US-196820P.	
PR	18-APR-2000; 2000US-198121P.	
PR	18-APR-2000; 2000US-198565P.	
PR	25-APR-2000; 2000US-199397P.	
PR	25-APR-2000; 2000US-199530P.	
PR	25-APR-2000; 2000US-199654P.	
PR	03-MAY-2000; 2000US-201516P.	
PR	17-MAY-2000; 2000WO-US13705.	
PR	22-MAY-2000; 2000WO-US14042.	
PR	30-MAY-2000; 2000WO-US14941.	
PR	02-JUN-2000; 2000WO-US15264.	
PR	05-JUN-2000; 2000US-209632P.	
PR	28-JUL-2000; 2000WO-US20710.	
PR	22-AUG-2000; 2000US-0644848.	
PR	24-AUG-2000; 2000WO-US23328.	
PR	08-NOV-2000; 2000WO-US30952.	
PR	01-DEC-2000; 2000WO-US32678.	
PR	20-DEC-2000; 2000WO-US34956.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,	
PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;	
XX		
DR	WPI; 2001-602746/68.	
XX	N-PSDB; AAS45941.	
XX		
PT	Novel nucleic acids encoding PRO polypeptides, used to diagnose the	
PT	presence of tumours, such as prostate and breast tumours, in mammals and	
PT	to screen for modulators of the compounds -	
XX		
PS	Claim 11; Fig 34; 774pp; English.	
XX		
CC	Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.	
CC	The PRO polypeptides and their associated nucleic acids can be used to	

CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

Sequence 440 AA;

Alignment Scores:	
Pred. No.:	2.8e-146
Score:	1741.00
Percent Similarity:	99.11%
Best Local Similarity:	98.81%
Query Match:	96.51%
DB:	22
Gaps:	0
Length:	440
Matches:	332
Conservative:	1
Mismatches:	3
Indels:	0

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAU29040 (1-440)

QY	1	ATCCCAACAGGTGATGGACACAAATCTGTTTACTTAAACAGCTGACAGTGGATTGAAGGAA	60
Db	37	IIlePrrthngIlyaspGlyGlnasnLeuPheThrIyaspValThrValIIleGlnGlyGln	56
QY	61	GTGGCAACCAATCAGCTGGCCAGGTCAATAAAGAGTGCACACATCAGATCCAGCTCTCAAC	120
Db	57	ValAlaThrIIleSerCysGlnValAsnIySerIaspSperValIIleGlnLeuLeuAsn	76
QY	121	CCCAACAGCAGACCAATTACTTCAGGGACTTCAGGCTTTGAAGCAGACAGGTTTCAG	180
Db	77	ProAsnArgGlnThrIIleTyrPheArgAspPheArgProLeuIySaspSerArgPheGln	96
QY	181	CTGCGAATTTTTCAGACAGTCAACTCAACTGACAGCAATGTCATCTCAATCTGGAT	240
Db	97	LeuLeuAsnPheSerSerSerGlnLeuIyValSerLeuThrAsnValSerIIleSerAsp	116
QY	241	GAAGGAGAACTACTTCGTGCACGCTTACACAGGACCCCCACAGAGAGATTAACACCACATC	300
Db	117	GlnGlyArgTyrPheCysGlnLeuTyrThrAspProArgGlnIySerTyrThrThrIle	136
QY	301	ACAGTCTGGTTCTCCACAGTACTTGATGATGATATCCAGAAGACACAGCAGTTGAA	360
Db	137	ThrValLeuValProProArgAsnLeuMetIleAspIIleGlnIySaspThrAlaValGln	156
QY	361	GGGGAGGAGATTGAAGTCAACTGACTGACCATGGCCAGCAAGCCAGGAGGACCAATCAG	420
Db	157	GlyGlnGlnIleGlnValAsnCysThrAlaMetAlaSerIySpproAlaThrThrIleArg	176
QY	421	TGGTTCAAAGGAAACAAGAACTCAAGAGCAAAATCAGAGGTGGAGAGTGGTGGCAATG	480
Db	177	TrpPheIySgIyAsnThrGlnLeuIyGclIySerGlnValGlnGlnIyTrpSerAspMet	196
QY	481	TACACTGTGACCACTCAGCTGATGCTTAAGGTGCACAGAGAGACAGGGGTCCGGGTG	540
Db	197	TyrThrValThrSerGlnLeuMetLeuIyValHisIySgIyAspSperValProVal	216
QY	541	ATTCGCCAGGTGGAGCAACCGCGCGTACATGAGAAACCTGCAGACCCAGCGCTTTCAGAA	600
Db	217	IIleCysGlnValGlnIySpproAlaValThrGlyAsnLeuGlnThrGlnArgIyTrleGln	236
QY	601	GTGCAGTATAAACCGCAAGTGCATATCCAGATGACTTACCCTCTGGAAAGGCCCTAACCCGG	660
Db	237	ValGlnTyrIySpproGlnValHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg	256
QY	661	GAAGGGATGCATTGTAGTTTACGTGTGAAGCAATCGGGAAGCCCAAGCCTGTGATGCTA	720

Db 257 GIUGLYASPALALEUCLUETHRCYSGIUALAIIIEGLYLYSPROGLINPROVALIMETVAL 276
OY 721 ACTGTCGTCAGAGTCGATGATGAATGCTCAACATCCGCTACTGTGGCCAAACCTG 780
Db 277 TTTCTPVALARGVALIASPSPILUMETPROGLINHLSALAVALLAUSERGILYPROASLEU 296
OY 781 TTCATCAATTAACCTTAACAAAACAGATTAACGGTACTACCGCTGTGAGGCTTCCAAACATA 840
Db 297 PHEIIASNAASNLASNLASNYSTRASPANGLYTHYTRARGCYSGIULASERASNILE 316
OY 841 GTGGGAAAGCTCATTCGACTATATGCTGTATGTATACGATCCCCCAACATATCCCT 900
Db 317 VALGILYLSALHISERASPYRMELEUTRYVALTYTRASPProthrrthrrillepro 336
OY 901 CCTCCACAACAACCAACCACTACACACACACACACACATCCTTACCATCATC 960
Db 337 PROProthrrthrrthrrthrrthrrthrrthrrthrrthrrilleuthrrille 356
OY 961 ACAGATTCGACGACGATGAAGGGGACCATTTGGGCGAGTGACAC 1008
Db 357 THRASPSErARGALAGLYGIUGLYSERILeARGALAVAlASPhts 372
RESULT 6
AAB25619
ID AAB25619 standard: Protein; 442 AA.
XX
AC AAB25619:
XX
DT 21-NOV-2000 (first entry)
XX
DE Protein encoded by human secreted protein gene #11.
XX
KM Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KM antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
KM anticancer; vulnerary; antiviral; antibacterial; antifungal;
KM Immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KM multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KM Crohn's disease; nephritis; hyperproliferative disorder;
KM cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KM melanoma; lymphoma; wound healing; human.
XX
KM
OS Homo sapiens.
XX
PN WO200029435-A1.
XX
PD 25-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US25031.
XX
PR 28-OCT-1998; 98US-0105971.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI NI J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Mel Y;
PI Greene JM;
PI WPI: 2000-387742/33.
XX
DR
PT Isolated nucleic acid molecules encoding human secreted proteins are
PT used for the prevention, amelioration and treatment of autoimmune,
PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
PT wounds, and infectious diseases -
XX
XX
PS Disclosure: Page 182-183; 803pp; English.
XX
XX The present invention relates to 12 secreted human proteins and the
XX nucleotide sequences encoding them. The polynucleotide sequences given
XX in AAB0066-A80623 encode the 12 secreted protein sequences given in
XX AAB5576-B25593. The human secreted proteins have various activities
XX dependent on the tissues in which they are expressed. Examples of the
XX activities of the proteins include: immunosuppressant;
XX anti-inflammatory; antirheumatic; antineurotic; dermatological;
XX antiproliferative; antiarteriosclerotic; anticancer; vulnerary;

CC antiviral; antibacterial; and antifungal activity. The proteins,
CC polypeptides, agonists and antagonists may be used to treat prevent
CC and/or diagnose various disease, disorders and conditions examples of
CC which include: immune disorders e.g. Addison's disease, rheumatoid
CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
CC hyperproliferative disorders such as paraproteinleukemia and psoriasis;
CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
CC sequences may also be used in wound healing and the treatment of
CC infectious diseases. The human secreted protein gene #11 and protein
CC sequences are represented in sequences AAB0616 and AAB25586. Sequences
CC AAB0677-A80682 represent genes related to the secreted protein gene#11.
XX
SQ Sequence 442 AA:
XX
Alignment Scores:
Pred. No.: 2 8e-146 Length: 442
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 21 Gaps: 0
US-09-778-187b-3_COPY_62_1069 (1-1008) x AAB25619 (1-442)
OY 1 ATCCCAACAGAGTCGATGACAGATCTGTTTACTTAAGACGTGACATGATTAAGAGAGA 60
Db 39 IIEProthrrGlyASpLylglnASnLeuPheThrrLysASpAlhrValIIIEGLIUGLY 58
OY 61 GTGGCAACCATCAGCTGCCAGGTCAATTAAGATGACGACTGATGCCAGCTCTGAMC 120
Db 59 VALAIAThrILISerCYSGIlnValASnLysSerASpSerValIIIEGlnLeuLeuASn 78
OY 121 CCCAAGCAGCAGCCATTACTTCAGGAGCTTCAGGCTTTGAAGAGCAGCAGCTTTCAG 180
Db 79 ProASnArgInThrrLleYrrPheArgASpPheArgProLeuLysASpSerArgPheGln 98
OY 181 CTGCTGAATTTTCTAGCAGTGAACCTCAAGTCTCAGCAATGCTCAATCTCGAT 240
Db 99 LeuLeuASnPheserSerSerGluLeuLysValSerLeuThrrASnValSerILISerASp 118
OY 241 GAAGGAGATACTTCTGCCAGCTCTACAGGAGCCCCCAGAGAGATTACACCATTC 300
Db 119 GIUGLYArgTYrPheCYSGIlnLeuTYrrThrASpProProGlnLISerTYrrThrrIle 138
OY 301 ACAGTCCTGTCCTCCTCAGCATTAATGATGATGATGATATCCAGAAACACAGCGATTTGAA 360
Db 139 ThrValLeuValProProArgASnLeuMetILIASpILIEGlnLysASpThrrAlaValGln 158
OY 361 GGGAGAGAGATTGAAGTCAACTGTACTGCCATGCGCAGCAAGCCAGCAGCATTCAG 420
Db 159 GIUGLYGlnIIIEGLInValASnCYStrhrrAlaMetLALISerLysProAlhrThrrIleArg 178
OY 421 TGGTTCAAAAGGCAACAGAACTCAAGCAATCAAGAGGTGAGAGTGTGGACATG 480
Db 179 TrpPheLysGILYASnThrrLLeuLysGILYsSerGILValGlnLInThrrSerASpMet 198
OY 481 TACACTGTACACAGTATGATGATGCTGAAGGTGCACAAAGAGAGAGACGGGGTCCGGTG 540
Db 199 TYrrThrrValThrSerILInLeuMetLysValHISLysGlnASpASpLylValProVal 218
OY 541 ATCTGCCAGTGGAGACCCCTCGGTCACTGTGAAACCTGCAGACCCAGCGCTATTAGAA 600
Db 219 IIECYSGIlnValGlnHISProAlaValThrrGlyASnLeuGlnThrrLInrTYrrLeuGln 238
OY 601 GTGCACTATAAACCGCAAGTCATATCCAGATGACTTACCCTGTGCAAGCCATAACCCG 660
Db 239 VALGlnTYrrLysProGlnValHISILIEGlnMetThTYrProLeuGlnGILYLeuThrArg 258
OY 661 GAAGGAGATGCAATTTGAAGCTGAAGCATGGGAGAGCCCAAGCTGTGATGATGTA 720
Db 259 GIUGLYASPALALEUCLUETHRCYSGIUALAIIIEGLYLYSPROGLINPROVALIMETVAL 278

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QY 721 ACTTGGGTGAGACTGATGATGAATGCCCTCAACATGCCCTACTGCTGGCCCAACCTG 780
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QY 781 TTCATCAATTACTTAACAAACAAACAGATACGGTACTTACCGCTGTGAGCCTCCACATA 840
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Db 299 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGluAlaSerAsnIle 318
QY 841 GTGGGAAGGCTCATTCGCGCTATATGCTATATGATATACATGCCCCACACACTATCCCT 900
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Db 319 ValGlyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProPheThrIlePro 338
QY 901 CCTGCCACAACACACACACACACTACACACACACACACACACACATCTTACCATCATC 960
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Db 339 ProPheThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIle 358
QY 961 ACGAATTCGACGACGATGGAAGGAGGACCATTTGGGCGAGTGACAC 1008
    |||
Db 359 ThrAspSerArgAlaGlyGluGlySerIleArgAlaValAspHis 374

RESULT 7
AAy94341
ID AAy94341 standard; Protein; 442 AA.
XX
AC AAy94341;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human cell surface receptor protein #8.
XX
KW Human; HCSR; cytosstatic; antiarthritic; antirheumatic; antiasthmatic;
KW immunosuppressive; antiarteriosclerotic; antibacterial; antiarasitic;
KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia;
KW melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia;
KW Alzheimer's diseases; multiple sclerosis; epilepsy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide
    1..44
    /label= Signal_peptide
    45..442
    /label= HCSR-8
    57..126
    /label= Immunoglobulin_domain
    159..222
    /label= Immunoglobulin_domain
    260..315
    /label= Immunoglobulin_domain
    375..394
    /label= Transmembrane_domain
    53
    /note= "potential phosphorylation site"
    67
    /note= "potential glycosylation site"
    101
    /note= "potential glycosylation site"
    103
    /note= "potential phosphorylation site"
    113
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    155
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    /note= "potential phosphorylation site"
    176
    /note= "potential glycosylation site"
    190
    /note= "potential phosphorylation site"
    233
    /note= "potential phosphorylation site"
    Region

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FT FT /note= "potential phosphorylation site"
FT FT 241
FT FT /note= "potential phosphorylation site"
FT FT 304
FT FT /note= "potential glycosylation site"
FT FT 308
FT FT /note= "potential glycosylation site"
FT FT 310
FT FT /note= "potential phosphorylation site"
FT FT 329
FT FT /note= "potential phosphorylation site"
FT FT 368
FT FT /note= "potential phosphorylation site"
FT FT 432
FT FT /note= "potential glycosylation site"
PN MO200028032-A2.
XX
XX 18-MAY-2000.
PD
XX
PF 12-NOV-1999; 99MO-US26742.
XX
PR 12-NOV-1998; 98US-0191280.
PR 07-DEC-1998; 98US-0206647.
PR 08-MAR-1999; 99US-0123404.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
PI Hillman JL, Bandman O, Azimzal Y, Au-Young J;
XX
DR MPI: 2000-376546/32.
DR N-PSDB; AAA27051.
XX
PT New human cell surface receptor protein and polynucleotide useful for
PT diagnosis, prevention and treatment of cancer, immune disorders,
PT infection and neuronal disorders
XX
PS Claim 1; Page 81-82; 97pp; English.
XX
CC The present sequence is a novel human cell surface receptor protein
CC (HCSR) designated HCSR-8. The nucleotide sequence was identified in
CC Incyte Clone 312256 from the cDNA library LUNGNOT02, which was made from
CC RNA isolated from lung tissue. A number of Incyte Clones were used to
CC assemble the consensus sequence. BLAST analysis showed that the sequence
CC is homologous to immuno-superfamily protein B12 g3779242. HCSR and its
CC antagonist are useful for preventing or treating disorders associated
CC with decreased or increased expression or activity of HCSR. Such
CC disorders include cancers such as leukaemia and melanoma, immune
CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
CC bacterial and parasitic infections and neuronal disorders such as
CC akathesia, Alzheimer's disease, multiple sclerosis and epilepsy.
CC polynucleotides encoding HSCRs may be used as hybridisation probes to
CC diagnose these conditions. Anti-HCSR antibodies may be used as
CC antagonists, as a targeting or delivery mechanism for bringing
CC pharmaceutical agents into contact with cells or tissues expressing
CC HCSR and for diagnosis of HCSR-related disorders. HCSR and its
CC catalytic or immunogenic fragments are useful for drug screening using
CC libraries of compounds.
XX
SQ Sequence 442 AA;
XX
Alignment Scores:
Pred. No.: 2,8e-146 Length: 442
Score: 1741.00 Matches: 332
Percent Similarity: 99.11% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 3
Query Match: 96.51% Indels: 0
DB: 21 Gaps: 0
US-09-778-187B-3_COPY_62_1069 (1-1008) x AAy94341 (1-442)
QY 1 ATCCCCACAGGTGATGACAGAAATCTGTTACTTAAGACGTGACAGTGAATTGAAGAGAA 60

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39 ILEPRTHTGLYASPGLYGInAsnLeuPheThrLysAspValThrValIleGluGlu 58
61 GTGGACACCATAGCGTCGAGCATATAGAGTGCAGCATCGTGTATCCAGCTCCGCAAC 120
59 VALAIAthrlIleSerCysGlnValAsnLysSerAspAspSerValIleGlnLeuLeuAsn 78
121 CCCAACAGGCACACCATTTACTTTCAGGGCACTTCAGGCCCTTTGAGGACAGCAGGTTTCAG 180
79 PROAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 98
181 CTGCTGATTTTTCAGCAGTGAAGTCAAGTGTCACTGACAGAAATGTCATTCGCGAT 240
99 LeuLeuAsnPheSerSerSerGluLeuLysValSerLeuThrAspValSerIleSerAsp 118
241 GAAAGGAGATATTCTGCGCAGCTTACACGGACCCCGCCAGAGAGATACACCAACATC 300
119 GUGLGLYHrGTYrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 138
301 ACAGTCTGCTTCTCTCACAGTGAAGTGAATGATGATTCGATATCCAGAAACACAGCGCAGTTGAA 360
139 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 158
361 GGGGAGAGATTTGAAGTCACTGTACTGCCATGCGCAGCAGCAGCAGCAGCATCAG 420
159 GUGLGLYHrIleGluValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg 178
421 TGGTTCAAAGGAGACAGAGACTCAAGGCAATGACAGATGAGAGAGTGGCGAGATG 480
179 ThrPheLysGlyAsnThrGlyLeuLysGlyLysSerGlnValGlnIleThrPheSerAspMet 198
481 TACACTGTGACCAAGTCAAGTGAAGTGAAGTGCACAAAGAGAGAGACAGCGGTCCCGGTG 540
199 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspAspGlyValProVal 218
541 ATCTGCGCAGGTGAGACACCTCGCGTCACTGGAACCTGCAGACCCAGCGCTATCTAGAA 600
219 ILeCysGlnValGlnHisPheAlaValThrGlyAsnLeuGlnThrGlnArgTyrLeuGln 238
601 GTGCAGTATTAACCGCAAGTGCATATCCAGATGACTTACCGTCTGCAAGCGCTCAACCGCG 660
239 VALGlnTyrLysProGlnValHisIleGlnMetThrTyrProLeuGlnIleLysLeuThrArg 258
661 GAAGGGAGTCAATTGAGTTAACTGTGTGAAGCCATCGGAGAGCCCGCAGCTGTGATGTA 720
259 GUGLGLYAspAlaLeuGluLeuThrCysGlnAlaIleGlyLysProGlnProValMetVal 278
721 ACTGGGTGAGAGTGAAGTGAATGCTCAACATGCCGTACTGTGCGCCAAACCTG 780
279 ThrTyrValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu 298
781 TTCATCAATTAACCTAAACAAACAGATAAGGTAAGTACTACCGGTGAGGCTTCCAAACATA 840
299 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGlnLysAspSerAsnIle 318
841 GTGGAAAGGCTCATTCGAGTATATGCTGTATGTATACGATCCCCCAACATATCCCT 900
319 VALGlnLysAlaHisSerAspTyrMetLeuTyrValTyrAspProGlnThrThrIlePro 338
901 CCTGCCAACAACAACCAACCACTACACACACACACACACACATCCTTACCATATC 960
339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 358
961 ACAGATTTCTGAGAGAGTGAAGGAGGAGCATTTGGGCGAGTGAGCAC 1008
359 ThrAspSerArgAlaGlyGlnGlySerIleArgAlaValAspHis 374

RESULT 8
AAV45092
ID AAV45092 standard; Protein: 442 AA.
XX
AC AAV45092;
XX

31-MAY-2000 (first entry)
Human Lymphoid derived dendritic cell adhesion molecule.
Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
biological activity; quality control reagent; treatment; inflammation;
immune system disorder; autoimmunity; viral infection; infectious disease;
organ transplant rejection; bone marrow; modulator; immune response.
Homo sapiens.
Key Location/Qualifiers
Domain 1..374 /Label= Extracellular_domain
Peptide 1..38 /Label= Leader_peptide
Protein 39..442 /Label= Mature_human_LDCAM_polypeptide
Modified-site 67..69 /note= "N-Glycosylation site"
Modified-site 101..103 /note= "N-Glycosylation site"
Modified-site 113..115 /note= "N-Glycosylation site"
Modified-site 165..167 /note= "N-Glycosylation site"
Modified-site 304..306 /note= "N-Glycosylation site"
Modified-site 308..310 /note= "N-Glycosylation site"
Modified-site 375..395 /note= "N-Glycosylation site"
Domain /Label= Transmembrane_domain
Domain 396..442 /Label= Cytoplasmic_domain
WO200008158-A2.
17-FEB-2000.
05-AUG-1999; 99WO-US17905.
07-AUG-1998; 98US-0095672.
(IMMEX) IMMUNEX CORP.
Baum PR, Fanslow WC;
WPI: 2000-205712/18.
DR N-PSDB: AA250882.
XX
PT Novel molecules designated LDCAM are capable of altering or modulating
T cell function
XX
PS Claim 7; page 42-43; 44pp; English.
XX
CC The present amino acid sequence is the human lymphoid derived dendritic
cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
region of B7-1. Human LDCAM is expressed in breast, retina, foetal
liver, spleen and heart, lung, muscle, placenta, thyroid and lung
carcinoma. LDCAM polypeptides interacts with T cell surface molecules
to alter signalling and inhibits T cell proliferation, bind to
themselves and B7-1, an LDCAM binding protein and increases natural
killer (NK) cell populations. It may be used to measure the biological
activity and as quality control reagents of LDCAM binding proteins.
LDCAM may be used for treating disorders associated with malfunctioning
of immune system, inflammation, autoimmunity disorders, viral infected
cells, infectious diseases and for killing tumour cells. They are also
useful for prevention or reducing the effect of organ and bone marrow
transplant rejection and for modulating T cell immune responses. LDCAM
polypeptides may also be used as carriers for delivering agents attached
to T cells or cells bearing B7-1.

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XX Sequence      442 AA:
SQ
Alignment Scores:
Pred. No.:      2,8e-146      Length:      442
Score:          1741.00      Matches:      332
Percent Similarity: 99.11%      Conservative: 1
Best Local Similarity: 98.81%      Mismatches: 3
Query Match:    96.51%      Indels:      0
DB:            21      Gaps:      0

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAY45092 (1-442)

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QY 61 GTGGCAACCTTCAGCTGCCAGGTCAATAGAGTACAGTCTGATCCAGCTCTGAA 120
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Db 59 ValAlaThrlIeSerCysGIuValAsnLYsSerAspSerValIleGIuLeuAsn 78
QY 121 CCCACAGCAGACCAATTACTTACAGGACTTCAGGCTTGAAGCAGACAGTTTCAG 180
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Db 79 ProAsnArgGIuThrlIeYrPheArgAspPheArgProLeuLYsAspSerArgPheGIu 98
QY 181 CTGCTGAATTTTCTAGACAGTCACTCAAGTGTCACTGACGAATGTCTCAATCTCGAT 240
   |||
Db 99 LeuLeuAsnPheserSerSerGIuLeuLYsValSerLeuThrAsnValSerIleSerAsp 118
QY 241 GAAGGAGATATCTTCCAGCTCTACACGACCCGCCACAGAGAGTTACACCACCATC 300
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Db 119 GIuGIyArGIyTrPheCysGIuLeuYrThrAspProGIuInLYsSerYrThrThrlIe 138
QY 301 ACAGTCTGCTGCTCCACAGTAACTGATGATGATTCAGAAAGCAGCGGAGTTGAA 360
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Db 139 ThrValLeuValIProProArgAsnLeuMetIleAspIleGIuInLYsAspThrAlaValGIu 158
QY 361 GGGGAGAGATTTGAAGTCAACTGTACTGCCATGCCAGCAGACGACGACCATCAG 420
   |||
Db 159 GIyGIuGIuIleGIuValAsnCYsThrAlaMetAlaSerLYsProAlaThrlThrlIeArg 178
QY 421 TGGTTCAAGGGAACAAGCAACTCAAGCAATTCAGAGTGGAGAGTGTGGCATG 480
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Db 179 TrPheLYsGIuAsnThrGIuLeuLYsGIuLYsSerGIuValIleGIuInLYsSerAspMet 198
QY 481 TACACTGTGACAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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Db 199 TyrThrValIleThrSerGIuLeuMetLeuLYsValIleIleLYsGIuAspGIyValIProVal 218
QY 541 ATCTGCCAGGTGAGACACCTGGGTCACTGGAACCTGCAGACCGCATCTAGAA 600
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Db 219 IleCysGIuValIleGIuInLYsProAlaValThrGIyAsnLeuGIuInThrGIuInArgLYsLeuGIu 238
QY 601 GTCCATATTAACCGCAAGGCAATCCAGATGATCTTACCCTGTCAAGGCTTACCCG 660
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Db 239 ValGIuInLYsProGIuValIleIleGIuInLYsMetThrTYrProLeuGIuInLYsLeuThrArg 258
QY 661 GAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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Db 259 GIuGIyAspAlaLeuGIuLeuThrCYsGIuValAlaIleGIyLYsProGIuInProValMetVal 278
QY 721 ACTTGGGTGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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Db 279 ThrTrpValArgValAspArgIuMetProGIuInIleAlaValIleuSerGIyProAsnLeu 298
QY 781 TTCATCAATTAACCTTAACAACAACAGATAACGATTAACCGCTGTAGAGGCTTCAACATA 840
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Db 299 PheIleAsnAsnLeuAsnLYsThrAspAsnGIyThrTYrArgCysGIuAlaSerAsnIle 318
QY 841 GTGGGAAGGCTCATTCGAGCTATATGCTGATGATGATGATGATGATGATGATGATGAT 900
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Db 319 ValGIyLYsAlaIleIleSerAspTYrMetLeuTYrValTYrAspProThrThrlIlePro 338

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QY 901 CTTCCACACACACACACACACACTACACACACACACACACACACATCTTACCATC 960
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Db 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 358
QY 961 ACAGATTTCTGAGCAGGTGAAGAGGAGCATTGGGACATGACACAC 1008
   |||
Db 359 ThrAspSerArgAlaGIyGIuGIySerIleArgAlaValAspHis 374

RESULT 9
AAEI9887
ID AAEI9887 standard; Protein: 442 AA.
XX
AC AAEI9887;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
XX
KW Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KW liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200214557-A1.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25690.
XX
PR 15-AUG-2000; 2000US-225264P.
XX
PA (UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Reeves RH, yoshimori M:
XX
DR WPI; 2002-241913/29.
XX
PT Detecting cell proliferative disorder associated with tumor suppressor
PT lung cancer (TSLC1) I in subject, comprises contacting proliferating
PT cell of subject with reagent detecting TSLC1 and detecting modification
PT in TSLC1 level -
XX
PS Disclosure; Page 49-50; 59pp; English.
XX
CC The invention relates to a method for detecting cell proliferative
CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a
CC subject. The method comprising contacting a cell component of a
CC proliferating cell with a reagent that detects level of the cell
CC component in the proliferating cell and determining modification in the
CC level of the cell component in proliferating cell as compared with a
CC healthy cell, where modification indicates disorder associated with
CC TSLC1. The method is useful for detecting a cell proliferative disorder
CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
CC therapy and for treating a cell proliferative disorder such as lung
CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
CC carcinoma) or pancreatic cancer associated with modification of TSLC1
CC production, where a reagent which modulates (preferably, increases) TSLC1
CC level in the cells, is employed. The present sequence is human TSLC1.
XX
SQ Sequence      442 AA:
Alignment Scores:
Pred. No.:      2,8e-146      Length:      442
Score:          1741.00      Matches:      332
Percent Similarity: 99.11%      Conservative: 1
Best Local Similarity: 98.81%      Mismatches: 3
Query Match:    96.51%      Indels:      0
DB:            23      Gaps:      0

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAEI9887 (1-442)

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OY 1 ATCCCAAGAGTGTGAGAGATCTGTTTAAAGACCTGACAGTATGAGAGAA 60
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OY 61 GAGGCAACATGAGTGGAGGTCATAGAGAGACAGTGTATCCAGGTCCTGAAC 120
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Db 59 ValAlaThr1IleSerGlnValAsnLysSerAspAspSerVal1IleGlnLeuLeuAsn 78
OY 121 CCCAACAGGACAGACATTTACTTACAGGACCTTACAGGCTTTGAAGACAGACAGTTTCAG 180
   |||
   |||
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Db 79 ProAlaArgGlnThrIleThrLeuArgAspPheArgProLeuLysAspSerArgPheGln 98
OY 181 CTGCTGAATTTTCTTACAGAGTACACCAAGTGTCTACACCAATCTCAATCTGGAT 240
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Db 99 LeuLeuAsnPheSerSerSerGluLeuLysValSerLeuThrAsnValSer1IleSerAsp 118
OY 241 GAAGGAGATTAATCTTGCAGGCTCTACAGGACCCCGCCAGAGAGATTACACACCATC 300
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Db 119 GluGluArgTyrPheCysGlnLeuTyrThrAspProProGlnLysSerTyrThrThrIle 138
OY 301 ACAGTCCCTGGTTCCCTCCAGCTAATCTGATGATGATATCCAGAAAGACAGCGAGTTGAA 360
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   |||
Db 139 ThrValLeuValProProArgAsnLeuMet1IleAsp1IleGlnLysAspThrAlaValGlu 158
OY 361 GGGGAGACATTTGAAGTCAACTGTACTGCCATGCGCCAGACAGCGACAGCATCAGG 420
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   |||
   |||
Db 159 GlyGluGlu1IleGluValAsnG1nSerThrAlaMetAlaSerLysProAlaThrThrIleArg 178
OY 421 TGGTTCAAGGGAACAGAACTCAAGCAATCAAGTGAAGAGAGAGTGGAGAGTGGTGGACATG 480
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Db 179 ThrPheLysG1yAsnThrGluLeuLysG1yLysSerGluValG1u1uThrPheSerAspMet 198
OY 481 TACACTGTGACAGAGTACAGTGTGTAAGGTGTGCACAGAGAGAGACAGCGGGTCCCGGTG 540
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Db 199 TyrThrValThrSerGlnLeuMetLeuLysVal1HisLysGluAspArgValProVal 218
OY 541 ATCTGCCAGGTGAGACACCTGGGTCACATGGAAACCTGCAGACCCGAGCTATCTAGAA 600
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   |||
Db 219 IleCysGlnValG1nHisProAlaVal1ThrG1yAsnLeuGln1nThrG1nArgTyrLeuGln 238
OY 601 GTCAGATTAATCAAGGAGTGCATATCCAGATCACTTACCCTGTGAGAGGCTTAAACCCG 660
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Db 239 ValGlnTyrLysProGlnVal1His1IleGlnMetThrTyrProLeuGlnGlyLeuThrArg 258
OY 661 GAAGGGATGCATTTGAGTTAAGCTGTGAAGCCATGCGGAAAGCCAGCCGTGATGATA 720
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Db 259 GluG1yAspAlaLeuGluLeuThrCysGluAla1IleG1yLysProGlnProValMetVal 278
OY 721 ACTTGGGTGAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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Db 279 ThrThrValArgValAspAspArgLysMetProGlnHisAlaVal1LeuSerGlyProAsnLeu 298
OY 781 TTCATCAATTAACCTTAACAAACAGATTAACGGTACTTACCGGTGAGGCTTCAACATA 840
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Db 299 Phe1AsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgGlySerLysAlaAspAsn1Ile 318
OY 841 GTGGGAAGGCTCATTCGAGTATATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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Db 319 ValGlyLysAlaHisSerAspArgLysMetLeuTyrValTyrAspProProThrThrIlePro 338
OY 901 CCTCCCAACAACAACACCACTACACACACACACACACACACACACATCCTTACCATCATC 960
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   |||
Db 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIle 358
OY 961 ACAGATTTCTGAGCAGTGAAGAGGAGACATTTGGGCGAGTGCACAC 1008
   |||
   |||
   |||
Db 359 ThrAspSerArg1aG1yGluGluGlySer1IleArg1aValaAspHis 374

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RESULT 10
 AAB25586
 ID AAB25586 standard; Protein: 364 AA.
 XX
 AC AAB25586;

XX 21-NOV-2000 (first entry)
 DT
 XX Protein encoded by human secreted protein gene #11.
 DE
 XX
 XX
 KW Secreted protein; immunosuppressant; anti-inflammatory; antirheumatic;
 KW antirheumatic; dermatological; antiproliferative; antiatherosclerotic;
 KW anticancer; vulnery; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human.
 KM
 OS Homo sapiens.
 XX
 PN MO200029435-A1.
 XX
 PD 25-MAY-2000.
 XX
 XX 27-OCT-1999; 99WO-US25031.
 PF
 XX 28-OCT-1998; 98US-0105971.
 PR
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI
 PI M J, Ruben SM, Olsen HS, Young PE, Kenny J, Moore PA, Wei Y;
 PI Greene JM;
 XX
 DR MPI: 2000-387742/33.
 DR N-PSDB: AAB80616.
 XX
 XX Isolated nucleic acid molecules encoding human secreted proteins are
 PT used for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases -
 PT
 XX
 PS Claim 1: Figure 28A-B; 803pp; English.
 XX
 CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given
 CC in AAB80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant;
 CC anti-inflammatory; antirheumatic; antiatherosclerotic; antitumor;
 CC antiproliferative; antiatherosclerotic; anticancer; vulnery;
 CC antiviral; antibacterial; and antifungal activity. The proteins,
 CC polypeptides, agonists and antagonists may be used to treat prevent
 CC and/or diagnose various disease, disorders and conditions examples of
 CC which include: immune disorders e.g. Addison's disease, rheumatoid
 CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
 CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
 CC hyperproliferative disorders such as paraproctanemias and purpura;
 CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
 CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
 CC sequences may also be used in wound healing and the treatment of
 CC infectious diseases. The human secreted protein gene #11 and protein
 CC sequences are represented in sequences AAB80616 and AAB25586. Sequences
 CC AAB80677-A80682 represent genes related to the secreted protein gene#11.
 XX
 SQ Sequence 364 AA:
 XX
 Alignment Scores:
 pred. No.: 4e-142
 Score: 1694.00 Length: 364
 Percent Similarity: 99.38% Matches: 323
 Best Local Similarity: 99.38% Conservative: 0
 Query Match: 93.90% Mismatches: 2
 Indels: 0
 Gaps: 0
 DB: 21

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAB25586 (1-364)

```

QY 1 ATCCCCACAGGTGATGACAGAAATCTGTTTACTAAAGACGTGACAGTGAATGAAGAGAA 60
DB 39 ILeProThrlGlyAspGlyGlnAsnLeuPheThrLysAspValThrValIleGluGlu 58
QY 61 GTGGCAACCATTCAGTCCCGCGGTCAATAAGAGACACATCAGATCCAGCTCTCTAAC 120
DB 59 ValAlaThrIleSerCysGlnValAsnLysSerAspSerValIleGlnLeuAsn 78
QY 121 CCCAACAGCAGACCATTTCTCAGGAGCTTACAGCCCTTGAAGACACAGATTTCAG 180
DB 79 ProAsnArgLlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 98
QY 181 CTGCTGAATTTTCTAGACAGTGAATCAAGTGTCTACTGACGAATGTCTCAATCTCGAT 240
DB 99 LeuLeuAsnPheSerSerSerGlnLeuLysValSerLeuThrAsnValSerIleSerAsp 118
QY 241 GAAGGAGATCTTCTCCCGCTCTACACGACCCCGCCACAGAGAGATTACACCATC 300
DB 119 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrIle 138
QY 301 ACAGTCTCGTCTCCAGCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 360
DB 139 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnLysAspThrAlaValGlu 158
QY 361 GGGGAGAGATTTAAGTCAACTGACTGCGATGCGCCAGCAAGCCAGCAGCAGCATCAGG 420
DB 159 GlyGluGlnIleGlnValAsnLysThrAlaMetAlaSerLysProAlaThrThrIleArg 178
QY 421 TGGTTCAAGGAAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 480
DB 179 ThrPheLysGlnAsnThrGlnLeuLysGlyLysSerGlnValGluGluTyrPheAspMet 198
QY 481 TACACTGTGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 540
DB 199 TyrThrValThrSerGlnLeuMetLeuLysValHisLysLysLysAspGlyValProVal 218
QY 541 ATCTGCACAGGTGACAGACCTCGCGCTCACTGGAACCTGCAAGCCAGCCCTACTGAAGA 600
DB 219 IleCysGlnValGlnHisProAlaValThrGlyAsnLeuGlnThrGlnArgTyrLeuGln 238
QY 601 GTGCATATATTAACCCGCAAGGATATCCAGATGATGATGATGATGATGATGATGATGAT 660
DB 239 ValGlnThrLysProGlnValHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 258
QY 661 GAAGGGGATGATTTAGTTAAAGTGTGAAGCCATCGGAAGCCAGCCCTGTGATGTA 720
DB 259 GluGlyAspAlaLeuGlnLeuThrCysGlnAlaIleGlyLysProGlnProValMetVal 278
QY 721 ACTTGGGTGAGACTGATGATGATAATGCTCAACATGCGGTACTGTCTGGGCCAAACCTG 780
DB 279 ThrThrValArgValAspAspGlnMetProGlnHisAlaValLeuSerGlyProAsnLeu 298
QY 781 TTCATCAATTAACCTTAACAAACAGATAACGAGTACTTACCGCTGTAGAGTTCCACATA 840
DB 299 PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyrArgCysGlnAlaSerAsnIle 318
QY 841 GTGGGAAAGGCTCATTCGACATATATGCTGATGATGATGATGATGATGATGATGATGAT 900
DB 319 ValGlyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProProThrThrIlePro 338
QY 901 CCTCCCAACAACAACCAACCACTACACACACACACACACACACACACACCTTACATCAG 960
DB 339 ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIle 358
QY 961 ACAGATTCTCGAGCA 975
DB 359 ThrAspSerArgAla 363

```

RESULT 11
 AAB88427
 ID AAB88427 standard; Protein; 443 AA.
 XX
 AC AAB88427;

```

XX 23-MAY-2001 (first entry)
DT Human membrane or secretory protein clone P58C0200.
XX
DE Human; secretory protein; membrane protein; vaccine; gene therapy;
XX rheumatoid arthritis; diabetes.
XX
KW Homo sapiens.
XX
OS EP1067182-A2.
XX
PN 10-JAN-2001.
XX
PD 07-JUL-2000; 2000EP-0114090.
XX
PF 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
XX MPI; 2001-093989/11.
XX
XX N-PSDB; AAF93854.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development -
XX
XX Claim 1; SEQ ID 222; 609pp + CD ROM; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by
XX AAB88317 - AAB88419. Included in the invention are primers
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX cDNA sequences of the invention. The invention also includes methods for
XX the production of antibodies directed against the proteins, and cDNA
XX sequences, which can be used in vaccines. The polynucleotide sequences
XX can be used in gene therapy. The polynucleotide sequences and the
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with inappropriate secretory
XX protein/membrane protein expression. The nucleic acids and complementary
XX sequences may also be used as DNA probes in diagnostic assays
XX (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
XX presence of similar nucleic acid sequences in samples. They may also be
XX used to study the expression and function of secretory proteins/membrane
XX polypeptides and their role in metabolism. The polypeptides may be used
XX as antigens in the production of antibodies against them and in assays to
XX identify modulators (agonists and antagonists) of expression and
XX activity. The antibodies and antagonists may also be used as therapeutic
XX agents to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of the
XX polypeptides in samples (e.g. by enzyme linked immunosorbent assay
XX (ELISA). Examples of diseases which may be treated include rheumatoid
XX arthritis and diabetes.
XX
XX Sequence 443 AA:
SQ

```

Alignment Scores:
 Pred. No.: 4,54e-133 Length: 443
 Score: 1592.50 Matches: 308
 Percent Similarity: 92.88% Conservative: 5
 Best Local Similarity: 91.39% Mismatches: 23
 Query Match: 88.28% Indels: 1
 DB: 22 Gaps: 1

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAB88427 (1-443)
 QY 1 ATCCCCACAGGTGATGACAGAAATCTGTTTACTAAAGACGTGACAGTGAATGAAGAGAA 60
 DB 39 ILeProThrlGlyAspGlyGlnAsnLeuPheThrLysAspValThrValIleGluGlu 58

OY	61	GTGGCAACCATCAGCTGCCAGGTCAATTAAGACGTGACAGCATCTCACTGATCCAGCTCCGTGAC	120
Db	59	ValaIaThrIleSerCysGlnValaIasnIlySerAspAspSerValIleGlnLeuLeuAsn	78
OY	121	CCCAACAGCGGACCAATTAATCAAGGAGCTCGAGGCTTTGAAAGCACACAGGTTTCAG	180
Db	79	ProAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerValArgPheGln	98
OY	181	CTGCTGAATTTTCTAGCAGTGAACCTAAAGTGTCACTGACAGATGCTCAATCTGGAT	240
Db	99	LeuLeuAsnPheSerSerSerGlnLeuIlyValIserIleuThrAsnValIserIleSerAsp	118
OY	241	GAAGCGAGATACCTTCTGGACAGCTCTACAGGAGCCGCCACAGGAGATTACACACCATC	300
Db	119	GluGluArgTyrPheCysGlnLeuTyrThrAspProProGlnIuSerTyrThrIle	138
OY	301	ACAGTCCCGGTCTCTCCACGTAATTTATGATGATATCCAGAAAGACAGCGAGTTTGA	360
Db	139	ThrValLeuValProProArgAsnIleMetIleAspIleGlnLysAspThrValaGlu	158
OY	361	GGGGGAGGATTGAAGTCAACTGACTAGTCCATGGCCAGCAAGCCAGGACGACATCAG	420
Db	159	GlyGluGlnIleGluValaAsnCysThrAlaMetKAlaSerLysProAlaThrThrIleArg	178
OY	421	TGGTTCAAGGGAACAAAGAACTCAAGGCAAAATCAGAGGTGGAGAGTGGTGCGACATG	480
Db	179	TrpPheLysGluAsnThrGlnIleuLysGluLysSerGlnValGlnGluTyrPserAspMet	198
OY	481	TACAGCTGACCACTCAGCTGATGCTGAGGTGCSACAAGAGACAGCGGGTCCGGTG	540
Db	199	TyrThrValIThrSerGlnIleMetLeuLysValaIHisLysGlnAspArgGluValProVal	218
OY	541	ATGCGCCAGGAGGAGCAACCCGCGGTCACTGGAAACCTGGAGACCCGAGCCTATTGA	600
Db	219	IleCysGlnValGlnHisProAlaValaThrGlnLysLeuGlnThrGlnaGlyLeuGln	238
OY	601	GTCCAGTATTAACCCCAAGTGCATATCCATGATGACTTAACCTCTGCAAGGCTTAACCCCG	660
Db	239	ValGlnTyrGlnsProGlnValaIHisIleGlnMetThrGlyProLeuGlnGluLeuThrArg	258
OY	661	GAAGGGAGTGCATTTGAATTAACTGTGAAGCCATCGGAAAGCCCAAGCTGTGATGTA	720
Db	259	GluGluArgAlaLeuGlnIleuThrCysGlnValaIleGlyLysProGlnProValMetVal	278
OY	721	ACTTGGGAGAGAGTGCATGATGAATGCGCTCAACATCGGAGCTGTGGGCCAAACCTG	780
Db	279	ThrThrValaIArgValaAspAspGlnMetCProGlnHisValaIleuSerGlyProAsnLeu	298
OY	781	TTTCATCAATTAACCAACCAAAACAGATACAGGTCTTAACGCTGTGAGGCTTCAACATA	840
Db	299	PheIleAsnAsnLeuAsnLysThrAspAsnGlnYhrTyrArgCysGlnAlaIAspAsnIle	318
OY	841	GTGGGAAGGCTCATTTGGAGATATATGCTGTATGATATAGCATGCCCCCAACATATGCT	900
Db	319	ValGlyLysValaIHisSerAspTyrMetLeuTyrValaTyrAspThrThrAlaThrThrGln	338
OY	901	CTCTCCCAACAAACACACACACATACACACACACACACACACACACACACACACACAC	960
Db	339	ProAlaValaIHisGlyLeuThrGlnLeuProAsnSerIleActGluIleuAspSerGluAsp	358
OY	958	ATCAACAGATTCTCGACAGCTGAAGAGGAGCACTTGGGCGAGTGGACAC	1008
Db	359	LeuSerAspSerArgAlaGlyGlnGluGlnGlySerIleArgAlaValaAspHis	375
RESULT 12			
AAVS3028			
ID	AAVS3028	standard; Protein: 414 AA.	
AC	AAVS3028:		
XX			
DT	29-FEB-2000	(first entry)	
DE			
Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.			

XX XX Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; suppression;
KV haematopoiesis regulation; tissue growth; activin; inhibin;
KM chemorectic; chemokine; haemostatic; thrombolytic; receptor;
KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
XX tumour inhibition; gene therapy.
XX
OS Homo sapiens.
PN
MO957132-A1.
XX
PD 11-NOV-1999.
PF
07-MAY-1999; 99WO-US0970.
XX
PR 07-MAY-1998; 98US-0084564,
PR 02-JUN-1998; 98US-0087645.
PR 22-JUL-1998; 98US-0037712.
PR 31-JUL-1998; 98US-0094933.
PR 10-AUG-1998; 98US-0095880.
PR 11-AUG-1998; 98US-0096068.
PR 06-MAY-1999; 99US-0096068.
XX
PA (GENY) GENETICS INST INC.
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Moberg D, Treacy M, Agostino MJ, Steinger RJ, Bowman MR;
PI DiBastio-Smith E, Wildom A:
WPI: 2000-052937/04.
DR N-PSDB: AAZ33346.
XX
PT New polynucleotides encoding secreted human proteins, derived from
PT adult placenta, adult retina, fetal brain, fetal -
XX
PS Claim 71; Page 416-417; 492pp; English.

XX XX The present invention describes new human secreted proteins which were
CC isolated from adult placenta, adult retina, foetal brain, foetal kidney
CC adult blood, adult brain, adult thyroid, adult bladder, adult neural
CC tissue, adult testes, and adult lymph node cDNA libraries. The human
CC secreted proteins, and the polynucleotides encoding them, are predicted
CC to have biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals. Suggested activities include nutritional activity, cytokine
CC and cell proliferation/differentiation activity, immune stimulating
CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
CC activity, tissue growth activity, activin/inhibin activity,
CC chemorectic/chemokinetic activity, haemostatic and thrombolytic
CC activity, receptor/ligand activity, anti-inflammatory activity,
CC cadherin/tumour invasion suppressor activity, and tumour inhibition
CC activity. The polynucleotides are also stated to be useful for gene
CC therapy. AAZ33316 to AAZ33373 encode human secreted proteins, and
CC AAZ52998 to AAZ53060 represent human secreted proteins, given in the
CC present invention.
XX
SQ Sequence 414 AA;

Alignment Scores:

Pred. No.:	3,63e-131	Length:	414
Score:	1571.00	Matches:	304
Percent Similarity:	90.77%	Conservative:	1
Best Local Similarity:	90.48%	Mismatches:	3
Query Match:	87.08%	Indels:	28
DB:	21	Gaps:	1

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAY53028 (1-414)

QY 1 ATCCCCACAGGTGATGCACACAACTCTTTTACTTAAGAAGCGTGACGTGATTGAAGAGCAA 60
|||||
39 IIEPOTNGIYASGIGVINSINSEUPHERIRLYSASPVALTTHVAIIIGLIGUIGIU 58
|||||

```

OY 61 GTGGCAACATFCAGCTGCCAGGTCAATAGAGTGACGACTGATGATCCAGCTCTCGAAC 120
    |||
DB 59 ValAlaThrIleSerCysGlnValAlaSnIlySerAspSerValIleGlnIleLeuAsn 78
OY 121 CCACAGGAGAGACANTTCTCTCAGGAGCTTCAGGCTTGAAGGACACAGGTTTCAG 180
    |||
DB 79 ProasnArgGlnThrIleTyrPheArgAspPheArgProLeuYasPseArgPheGln 98
OY 181 CTGCTGAATTTTCTAGACATGAGTCAATCAAGTGTCAATGTCAGATGCTCATCTCGAT 240
    |||
DB 99 LeuLeuasnPheSerSerSerGluLeuIlyValSerIleuThrAsnValSerIleSerAsp 118
OY 241 GAAGGAGATACTTCTGCCAGCTCTACAGGACCCCCACAGAGAGTTACACACCATC 300
    |||
DB 119 GluGlyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrThrIle 138
OY 301 ACAGTCTGCTGCTCCAGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 360
    |||
DB 139 ThrValLeuValIProProAlaGlnLeuMetIleAspIleGlnIlySasPThrAlaValGln 158
OY 361 GGGGAGAGATTAAGTCAACTGACTACTGCTCCATGAGCCAGCAAGCCAGGACCATCAG 420
    |||
DB 159 GlyGluGlnIleGluValAlaSnCysThrAlaMetAlaSerIlySProAlaThrThrIleArg 178
OY 421 TGGTTCAAGGGAACAAGAACTCAAAAGCAATCAGAGGTGAGAGTGTGGACATG 480
    |||
DB 179 TrpPheIlySglYasnThrGlnLeuIlySglYlySerGlnValGlnGlnIlyTrpSerAspMet 198
OY 481 TACACTGTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
    |||
DB 199 TyrThrValThrSerGlnIleMetLeuIlyValIlySglYlySasPArgIlyValIProVal 218
OY 541 ATCTGCCAGGTGAGACACCTGGGTCACTGGAACCTGAGAACCTGATCTAGAA 600
    |||
DB 219 IleCysGlnValAlaGlnIlySProAlaValIlyThrGlnIlySleuGlnIlyThrGlnIly 238
OY 601 GTCCAGTATTAACCCGCAAGTGCATATCCAGATGATGATGATGATGATGATGATGATGAT 660
    |||
DB 239 ValGlnIlySProGlnIlyValIlySleuMetThrIlyProIlyGlnIlyLeuThrArg 258
OY 661 GAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
    |||
DB 259 GluGlyAspAlaLeuGlnIleuThrCysGlnAlaIleGlyIlySProGlnIlyProValIlyMetVal 278
OY 721 ACTTGGGTGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
    |||
DB 279 ThrTrpValArgValAlaSerArgIlyMetProGlnIlyAlaValIleuSerGlyProAsnIleu 298
OY 781 TTGATCAATTAACCTAAACAACAACAAGATACGAGTACTTACCGCTGTGAGGCTTCCACATA 840
    |||
DB 299 PheIleAsnAsnIleuAsnIlySThrAspAsnGlyThrIlyArgCysGlnIlyAlaSerAsnIle 318
OY 841 GTGGGAAGGCTCATTCGCGCTATATGCTGATGATGATGATGATGATGATGATGATGATGAT 900
    |||
DB 319 ValGlyIlySAlaIlySerAspIlyMetLeuTyrValIlyTyr----- 331
OY 901 CCTCCCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 960
    |||
DB 331 ----- 331
OY 961 ACAGATTTCTGAGCAGGTGAGAGGAGGACCATTTGGGCGACTGAGACAC 1008
    |||
DB 332 ---AspSerArgAlaGlyGlnGlnIlySerIleArgAlaValAspHis 346

```

RESULT 13

AAB25593

ID AAB25593 standard; Protein: 229 AA.

AC AAB25593;

XX 21-NOV-2000 (first entry)

DE Protein encoded by human secreted protein gene #11 clone H0UDJ81.

```

XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; vulnary; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human.
OS Homo sapiens.
PN WO200029435-A1.
PD 25-MAY-2000.
PF 27-OCT-1999; 99MO-US25031.
PR 28-OCT-1998; 98US-0105971.
XX (HUMA-) HUMAN GENOME SCI INC.
XX NI J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
XX Greene JM;
XX MPI; 2000-387742/33.
XX
PT Isolated nucleic acid molecules encoding human secreted proteins are
PT used for the prevention, amelioration and treatment of autoimmune,
PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
PT wounds, and infectious diseases.
XX
PS Claim 1; Page 685-686; 803pp; English.
XX
CC The present invention relates to 12 secreted human proteins and the
CC nucleotide sequences encoding them. The polynucleotide sequences given
CC in AAB80606-A80623 encode the 12 secreted protein sequences given in
CC AAB25576-B25593. The human secreted proteins have various activities
CC dependent on the tissues in which they are expressed. Examples of the
CC activities of the proteins include: immunosuppressant;
CC anti-inflammatory; antiarthritic; antirheumatic; dermatological;
CC antiproliferative; antiarteriosclerotic; anticancer; vulnary;
CC antiviral; antibacterial; and antifungal activity. The proteins,
CC polypeptides, agonists and antagonists may be used to treat prevent,
CC and/or diagnose various diseases, disorders and conditions examples of
CC which include: immune disorders e.g. Addison's disease, rheumatoid
CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
CC hyperproliferative disorders such as paraproteinemia and purpura;
CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
CC sequences may also be used in wound healing and the treatment of
CC infectious diseases. The human secreted protein gene #11 and protein
CC sequences are represented in sequences AAB80616 and AAB25586. Sequences
CC AAB80677-A80682 represent genes related to the secreted protein gene#11.
XX
SQ Sequence 229 AA:

```

Alignment Scores:

Pred. No.: 2,49e-92 Length: 229
Score: 1133.50 Matches: 218
Percent Similarity: 96.48% Conservative: 6
Best Local Similarity: 96.04% Mismatches: 1
Query Match: 62.83% Indels: 2
DB: 21 Gaps: 1

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAB25593 (1-229)

OY 328 ATGATCGATATCCAGAAAGACGCGAGTTGAAGGGGAGAGATTGAAGTCAACTGACT 387
 |||
DB 1 MetIleAspIleGlnIlySasPThrAlaValGlnGlnIlyLeuValAlaSnCysThr 20
OY 388 GCCATGGCCAGCAAGCCAGCAGACCATTCAGGTGCTTCAAAAGCAACAAGAACTCAA 447

```
Db 21 AlMetAlaSerLysProAlaThrThrIleArgTrpPheLysGlyAsnThrClnLeuLys 40
Oy 448 GGCAGAAATGAGAGGAGAGAGTGGGACATGATACATGATGACAGTGCATGATGCG 507
Db 41 GilylssSerGlyValGlnClnTrpSerAspMetCylTrhValTrhSerClnLeuMetL 60
Oy 508 AAGGTGACAAAGAGAGAGAGGAGGAGTCCCGGTGATGTCGACAGTGCAGAGACCCGTC 567
Db 61 LysValAlHisLysGlnAspAspGlyValProValIleCysGlnValGlnHisProAlaVal 80
Oy 568 ACTGGAACCTGCACAGACCCGCTATGTAGAGTGCAGATTAACCGCACTGCATATC 627
Db 81 ThrGlyAsnLeuGlnThrClnArgTrpLeuGlnValGlnTrpLysProGlnValHisIle 100
Oy 628 CAGATGACTTACCCTCTCGAAGGCGCTAACCGGGAAGGAGGATTTGAGTTAAGTGT 687
Db 101 GlnMetTrhTrpProLeuGlnGlyLeuTrhArgGlnGlyAspAlaLeuGlnLeuThrCys 120
Oy 688 GAGGCAATCGGAGAGAGGAGGAGGAGTGTGATGATGATGATGATGATGATGATG 747
Db 121 GlnAlaIleGlyLysProGlnProValMetValTrhTrpValArgValAspAspGlnMet 140
Oy 748 CCTCAACATGCGGTACTGTCTGGGCCAAACCTGTTCATCATTAACCTAAACAAACAGAT 807
Db 141 ProGlnHisAlaValIleLeuSerGlyProAsnLeuPheIleAsnAsnLeuAsnLysThrAsp 160
Oy 808 AACGTTACTTACCCTGTCAGGCTGACGATCCAAACATAGTGGGAAGGCGATTCGAGATATAG 867
Db 161 AasnGlyTrhTrpArgCysGlnAlaSerAsnIleValGlyLysAlaHisSerAspTrpMet 180
Oy 868 CTGTATGTATACGATCCGCCACAACTATCCCTCTCCACAAACACACACACATACC 927
Db 181 LeuTrpValTrpAspProProTrhTrhIleProProTrhTrhIleProProTrhTrh 200
Oy 928 ACCACACACACACACACATCTTACATCATCATCATCATCATCATCATCATCATCAT 984
Db 201 ThrTrhTrhTrhTrhTrhTrhIleLeuThrIleIleThrAspSer-ProSerGlnValLysL 220
Oy 985 GGGACCATTTGGGGGAGTGG 1003
Db 220 SAlaArgSerGlyGlnTrp 226

RESULT 14
AAM78418
ID AAM78418 standard; Protein; 387 AA.
XX
AC AAM78418;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1080.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
```

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PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
DR MPI: 2001-476283/51.
DR N-PSDB: AAK51551.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 3307-3308; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.

SQ Sequence 387 AA:

Alignment Scores:
Pred. No.: 1,466-47 Length: 387
Score: 631.00 Matches: 124
Percent Similarity: 61.39% Conservative: 62
Best Local Similarity: 40.92% Mismatches: 111
Query Match: 34.98% Indels: 6
DB: Gaps: 3

US-09-778-187B-3_COPY_62_1069 (1-1008) x AAM78418 (1-387)
Oy 10 GGTGATGACAGAGATCTGTTACTTAAGAGTGCAGATGATGAAGAGAGAGTGCAGAC 69
Db 21 GylAlaGlyGlnGlnValGlnClnThrGlnAsnValThrValAlaGlnClnGlyAlaGln 40
Oy 70 ATCAGCTGCCAGGTCAATAGAGTACGACGATCAGTATCAGTATCAGTATCAGTATCAG 129
Db 41 IleThrCysArgLeuHisGlnTrpAspGlySerIleValValIleGlnAsnProAlaArg 60
Oy 130 CAGACCATTTACTTCAAGGAGTTCAGGCTTCCAGGCTTGAAGAGACAGAGTTCAGTGCAT 189
Db 61 GlnThrLeuPheAsnGlnGlyThrArgAlaLeuLysAspGlnArgPheClnLeuGlnGln 80
Oy 190 TTTTCTAGCAGTGAAGTCAAGAGTGTCACTGACGAAATGTCTCAATCTCGATGAAGGAGA 249
Db 81 PheSerProArgArgValArgIleArgLeuSerAspAlaArgLeuGlnAspGlnGlyGly 100
Oy 250 TACTTGTCCAGCTTACACGAGACCCGCCACAGAGAGTTCACACCCATCACAGTCTCG 309
Db 101 TyrPheCysGlnLeuTrpThrGlnAspTrhHisGlnIleAlaThrTrhLeuThrValLeu 120
Oy 310 GTTTCCTCCAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369
Db 121 ValAlaProGlnAsnProValValGlnVal--ArgGlnGlnAlaValGlnGlnGlnGln 139
Oy 370 ATTGAAGTCAAGTGTACTGCATGCGCAGACCAAGCAGCAGCAGTATCAGTGTGTTCAAA 429
Db 140 ValGlnLeuSerCysLeuValProArgSerArgProAlaIleThrLeuArgTrpTrpArg 159
Oy 430 GGCAGACAGAACTCAAGGCAATGACAGAGTGGAGGAGTGTGCGACATGTACACTGTG 489
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 20, 2002, 07:44:26 ; Search time 69.25 Seconds
(without alignments)
5998.426 Million cell updates/sec

Title: US-09-778-187B-3_COPY_62_1069

Perfect score: 1804
Sequence: 1 atccccacaggcgtatgacac.....ccattggggcagtgaccac 1008

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O/comp2.1/USPNC_SPOOL/US09778187/runat_20112002_073630_26319/app_query_fasta_1.2318
-DB=SPTRMBL_21 -QFMT=fascan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cgi -LIST=45
-DOCALLIGN=200 -THR_SCORE=DCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09778187.eccn.1.1.204@runat.20112002_073630_26319 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: SPTRMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	97.8	445	11	Q8R4L1 mus musculus

2	1749.5	97.0	456	11	Q8R5M8	Q8R5M8 mus musculus
3	1749.5	97.0	494	11	Q9CRY3	Q9CRY3 mus musculus
4	1738	96.3	442	4	Q9BY67	Q9BY67 homo sapien
5	1541	85.4	336	11	Q9D6E7	Q9D6E7 mus musculus
6	1204	66.7	295	11	Q9Z2H8	Q9Z2H8 mus musculus
7	1171.5	64.9	305	11	Q9QYL4	Q9QYL4 mus musculus
8	1151	63.8	295	11	Q9QYL6	Q9QYL6 mus musculus
9	1062	58.9	289	11	Q9QYL5	Q9QYL5 mus musculus
10	1038.5	57.6	278	11	Q9QYL3	Q9QYL3 mus musculus
11	624	34.6	388	11	Q8R4G4	Q8R4G4 mus musculus
12	611	33.9	381	4	Q9Y4A4	Q9Y4A4 homo sapien
13	480.5	26.6	396	11	Q99N28	Q99N28 mus musculus
14	467.5	25.9	432	4	Q9UPL1	Q9UPL1 homo sapien
15	298	16.5	549	11	Q9D006	Q9D006 mus musculus
16	296	16.4	510	11	Q9JL88	Q9JL88 mus musculus
17	295	16.4	549	11	Q9JL87	Q9JL87 mus musculus
18	294	16.3	438	11	Q9JL87	Q9JL87 mus musculus
19	289	16.0	549	4	Q9NDS3	Q9NDS3 homo sapien
20	261.5	14.5	5198	5	Q76518	Q76518 caenorhabd
21	252	14.0	439	13	Q57349	Q57349 gallus gall
22	252	14.0	1482	5	Q9V4Y0	Q9V4Y0 drosophila
23	245	13.6	407	4	Q9Y412	Q9Y412 homo sapien
24	238	13.2	725	13	Q73633	Q73633 xenopus lae
25	237	13.1	1102	11	Q9Z3W7	Q9Z3W7 mus musculus
26	234	13.0	393	4	Q95727	Q95727 homo sapien
27	228.5	12.7	7962	4	Q10465	Q10465 homo sapien
28	228.5	12.7	34350	4	Q8W442	Q8W442 homo sapien
29	226	12.5	4162	13	Q98918	Q98918 gallus gall
30	225	12.5	1032	13	Q8UVD6	Q8UVD6 brachydanio
31	222	12.3	725	13	Q73634	Q73634 xenopus lae
32	221	12.3	344	4	Q9P121	Q9P121 homo sapien
33	220.5	12.2	449	4	Q9UE16	Q9UE16 homo sapien
34	220	12.2	344	13	Q9DF61	Q9DF61 gallus gall
35	220	12.2	467	11	Q91V79	Q91V79 mus musculus
36	220	12.2	1675	13	Q98SM4	Q98SM4 brachydanio
37	219.5	12.2	1270	5	Q9J3P2	Q9J3P2 caenorhabd
38	219	12.1	344	11	Q99P00	Q99P00 mus musculus
39	219	12.1	1380	4	Q9HCK4	Q9HCK4 homo sapien
40	217.5	12.1	975	5	Q9J174	Q9J174 drosophila
41	217	12.0	417	4	Q96B01	Q96B01 homo sapien
42	216.5	12.0	605	4	Q96J84	Q96J84 homo sapien
43	216	12.0	1060	11	Q9QZ13	Q9QZ13 retus norv
44	215.5	11.9	1056	13	Q9QZ03	Q9QZ03 xenopus lae
45	215	11.9	4370	4	Q9H3V5	Q9H3V5 homo sapien

ALIGNMENTS

RESULT 1
ID Q8R4L1 PRELIMINARY: PRT: 445 AA.
AC Q8R4L1;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE Tumor suppressor in lung cancer 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT Identification of murine orthologs of the TSLC1 gene.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF344663; AAL86736.1; -;
SQ SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;

Alignment Scores:
Pred. No.: 2, 22e-146 Length: 445
Score: 1765.00 Matches: 336
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.84%	Indels:	0
DB:	11	Gaps:	0

US-09-778-187B-3_COPY_62_1069 (1-1008) x Q8R4L1 (1-445)

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Dd		42	IleProthrIglAspGlyglnAsnLeuPheThrLysAspValThrValIleGluGlyIu	61
OY		61	GTCGCAACCAATCAGCTGCCAGGTCAATAATGAAGTAGACAGCTCAGAGATCCAGCTCTAAC	120
Dd		62	ValAlaThrIleSerCysGlnValAsnLysSerLysPspSerValIleGlnIleLeuAsn	81
OY		121	CCCAACAGCAGACACCATTACTCTCAGGGCATTCAGGCCCTTTGAAGCAGACAGGTTTTAG	180
Dd		82	ProAsnArgIlnThrIleTyPheArgSpPheArgProLeuLysAspSerArgPheGln	101
OY		181	CTGGCGAATTTTTAGAGAGTAGACTCAAAATGTCACTGACGAGATGTCTCAATCCGAT	240
Dd		102	LeuLeuAsnPheSerSerSerGlnLeuLysValSerLeuThrAsnValSerIleSerAsp	121
OY		241	GAAGGAGATACTTCTGCGACCTCTACACGGAGCCCCACAGAGAGATTACACCAATC	300
Dd		122	GluGlyArgGyrPheCysGlnLeuTyThrAspProProGlnGlnSerTyThrThIle	144
OY		301	ACAGTCTCGGTCTCCACAGTAACCTTGATGATGATATCCAGAAAGACAGCGCAGTTGAA	360
Dd		142	ThrValLeuValProProArgAsnMetIleAspIleGlnLysAspThrAlaValGlu	161
OY		361	GGGAGAGGATTTGAAGTCAACTGACAGCCATGGCCAGCAAGCCAGGAGACCACTTACG	420
Dd		162	GlyGlnGluIleGluValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg	181
OY		421	TGGTTCAAAGGGAACAAGAACTCAAGGCAAAATCACAGGTGAGAGATGGTGACATG	480
Dd		182	TrpPheLysGlnAsnLysGlnLeuLysGlyLysSerGlnValGlnGluTrpSerAspMet	201
OY		481	TACACTGTGACCACTCAGCTGATCTCTAAGGTGCACAAGAGACAGCGGGTCCGGTG	540
Dd		202	TyThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspAspGlyValProVal	221
OY		541	AATGCCAGGSGAGSCACCCGCGGTACTGAGAAAACCTGGACGCCGCGCTTGTAGAA	600
Dd		222	IleCysGlnValGlnHisProAlaValThrGlyAsnLeuGlnThrGlnAlaGlyTyLeuGlu	241
OY		601	GTCGACGATTAACCCGCAAGTGCATATCCAGATGACTTACCCCTGCAGAGGCTTAACCCG	660
Dd		242	ValGlnTyLysProGlnValHisIleGlnMetThrTyProLeuGlnGlyLeuThrArg	261
OY		661	GAAGGGGATGATTTGAGTTAAGSTGAGAGCCATCGGGAAGCCCAGCGCTGTGATGTA	720
Dd		262	GluGlyAspAlaPheGluLeuThrCysGlnAlaIleGlyLysProGlnProAlaMetVal	281
OY		721	ACTTGGGTGAGAGTCGATGATGAATAAGCCCAACATCCCTACTGTCTGGGCAAACTG	780
Dd		282	ThrTrpValArgValAspAspGluMetProGlnHisAlaValLeuSerGlyProAsnLeu	301
OY		781	TTTATCAATAAATCAAAACAACAGATTAACGGTACTTACCGCTGTGAGGCTTCCAATA	840
Dd		302	PheIleAsnAsnLeuAsnLysThrAspAsnGlyThrTyArgGlyGlnAlaSerAsnIle	321
OY		841	GTCGGGAAGGCTAATCGGACTATATGCGTATGTAATACATCCCGCCCAACTATACCT	900
Dd		322	ValGlyLysAlaHisSerAspTyMetLeuTyValTyLysAspProThrThrIlePro	341
OY		901	CTTCCCAACAACAACAACCACTTACACACACACACACACACACACACATCCCTACATC	960
Dd		342	ProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIle	361
OY		961	ACAGATTCTGCAGCAGCTGAAGAAGGAGACCATTTGGGCACTGCAGCCAC	1008
Dd		362	ThrsPserArgAlaGlyGluGluGlyThrIleGlyValAlaLysPheS	377

RESULT 2			
Q8R5M8			
ID	Q8R5M8	PRELIMINARY;	PRT; 456 AA.
AC	Q8R5M8;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	RA175.		
GN	RA175.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Momoi T.;		
RT	"Biological function of RA175, a new member of immunoglobulin super		
RT	family."		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AB064265; BAB83501.2; -		
DO	SEQUENCE 456 AA; 49787 MW; 3226E8664ABC17F CRC64;		

Alignment Scores:			
Pred. No.:	5,13e-145	Length:	456
Score:	1749.50	Matches:	336
Percent Similarity:	96.83%	Conservative:	0
Best Local Similarity:	96.83%	Mismatches:	0
Query Match:	96.98%	Indels:	11
DB:	11	Gaps:	1
US-09-778-187b-3_COPY_62_1069 (1-1008) x Q8R5M8 (1-456)			
QY	1	ATCCCAACAGGTGATGACAGCAATCTGTTACTAAAGACGTGACGTGATTGAAGAGAA	60
Db	42	ILleProthrgIysaPglYgInAsnLeuPheThrIysaSpValThrValIIleGInGlu	61
QY	61	GTGGCAACCATCAGCTGCCAGGTAAATPAGTAGCAGCTAGTGATCCAGCTCTGAA	120
Db	62	ValAlaThrIleSerCysGInValAsnLysSeraspSerValIIleGInLeuAsn	81
QY	121	CCCAACAGCGACCATTTACTTAGGAGACTTCAGGCTTTGAAGAGACAGAGTTTCAG	180
Db	82	ProAsnArgGInThrIleTyrPheArgAspPheArgProLeuLysaspSerArgPheGIn	101
QY	181	CTGCTGAATTTTCTAGCAGTGAACCTAAAGTGTCACTGACGAATGTCTCAATCTCGAT	240
Db	102	LeuLeuAsnPheSerSerSerGluLeuLysValSerLeuThrAsnValSerIleSerAsp	121
QY	241	GAAGGAGATCTCTTCGCCAGCTTACACGGACCCCCACAGAGAGATTACACACATC	300
Db	122	GInGInIArgTyrPheCysGInLeuTyrThrAspProGInGInSerTyrThrIle	141
QY	301	ACAATCTCGTTCCTCCACAGTAACTGATGATTCAGATTCACAGAAAGACAGGAGTTGA	360
Db	142	ThrAlaLeuValProProAlaGlnLeuMetIleAspIleGInLysAspThrAlaValGlu	161
QY	361	GGGAGAGATTTGAAGTCAACTGACTGATGCCATGGCCAGCAAGCCAGGACCATCAG	420
Db	162	GlyGInGInIleGInValAsnCysThrAlaMetAlaSerLysProAlaThrThrIleArg	181
QY	421	TGCTTCAAAAGGAAACAGAACTCAAAAGCAATCAGAGTGGAGAGTGGTGGACATC	480
Db	182	TyrPheLysGlyAsnLysGluLeuLysGlyLysSerGluValGInGInTyrPheSeraspMet	201
QY	481	TACACTGTGACCACTGACGTGATGCTAAAGTGACGACAGAGAGACGAGGGGTCCGGTG	540
Db	202	TyrThrValThrSerGInLeuMetLeuLysValHisLysGInLysaspGlyValProVal	221
QY	541	ATCTGCAGGTGAGACCCCTGGCGTACTACGAAACCTGCAGACCCAGCGCTTCTAGAA	600
Db	222	ILleCysGInValGInHisProAlaValThrGlyAsnLeuGInThrGInArgTyrLeuGIn	241

QY 601 GTGACGTATAAACCGCAAGTCGATATCCAGATGACTTACCCTCTGCAAGCCCTAACCCGG 660
|||||
DB 242 VALGINTYLYSPROGLINVAIHSLIEGLIMETHTTYPROLEUCLINGLYEUTHRATG 261
QY 661 GAAGGGAGTCATTTGAGTTAAGCTGTGAAGCATTCGGGAAGCCCAAGCCTGTGATGTA 720
|||||
DB 262 GUGLYASPAIAPhEGLIUEUTHRCYSGIUALALEGLYLSYPROGLINPROVALMETVA 281
QY 721 ACTTGCGTGAGAGTCGATGATGAATGCTCTCAACATGCGCTACTGTCTGGCCAAACCTG 780
|||||
DB 282 THTTPVALATGVALASPAISPGIUMETCTROGLINHISALVALLEUSERLYPROKASNLEU 301
QY 781 TTCATCAATTAACCTTAACAAACAGATTAACGGTACTTACCCTGTGAGGCTTCCACATAT 840
|||||
DB 302 PHEILEASNPALAEUASNPILYSTRASPANSGLYTHRTTYARGCYSGIUALASERASNILE 321
QY 841 GTGGGAAGGCTCATTTGGGACATATATGCTGTATGCTATAGCATGCCCCCAACATACCTCT 900
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DB 322 VALGILYLSALAHISERASPTRYMETLEUTYVALTYTASPROPTHTHTTILEPRO 341
QY 901 CCTCCCAACAACACACACACACTACACACACACACACACATCCCTTACCATCATATC 960
|||||
DB 342 PROPTHT 361
QY 961 ACA-----GATTCCTGAGCAGGTGAAGGGG 987
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DB 362 THTTASPHTHTHTATHTHTHTHTGUPROALVALIHISAPSERATGALIEGLYUGIUGLY 381
QY 988 ACCATTGGGGCAGTGGACCAC 1008
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DB 382 THTTLEGLYALVALASPHIS 388
RESULT 3
O9CRY3 PRELIMINARY: PRT: 494 AA.
ID O9CRY3: 01-JUN-2001 (TREMBlrel. 17, Created)
AC O9CRY3: 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 31000011081K protein (Fragment).
GN IGSF4 OR 31000011081RK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa K., Nishi K., Kiyosawa H., Kondo S., Yamane A I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleschmann W., Gasteirland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK013911: BAB29050.1: -.
DR MGD: MGI:1889272: Igcf4.
DR InterPro: IPR003599: I9.
DR InterPro: IPR003598: Ig_c2.

DR InterPro: IPR003600: Ig_like.
DR InterPro: IPR003006: Ig_MHC.
DR Pfam: PF00047: I9: 3.
DR SMART: SM00409: IG: 3.
DR SMART: SM00408: IGC2: 3.
DR SMART: SM00410: IG_like: 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 494 AA: 53946 MW; F5E09ABA1857ABCO CRC64;
Alignment Scores:
Pred. No.: 5,21e-145 Length: 494
Score: 1749.50 Matches: 336
Percent Similarity: 96.83% Conservative: 0
Best Local Similarity: 96.83% Mismatches: 0
Query Match: 96.98% Indels: 11
DB: 11 Gaps: 1
US-09-778-187B-3_COPY_62_1069 (1-1008) x O9CRY3 (1-494)
QY 1 ATCCCCAGAGTGATGGAGAGAATCTGTTTACTAAAGAGTGACAGTGTGAAGAGAA 60
|||||
DB 80 ILEPTHTGLYASPOLYGLINSNPHEHTHTLYASPAVALTHRTVALILEGLUGLYGU 99
QY 61 GTGGCAACCATCATGCTGCAGGTCAATAAGATGACAGTCAAGTGTCCAGCTCTGAAC 120
|||||
DB 100 VALALATHTLTESERCYSGIUALASNPYLSERASPASERVALILEGLINLEUASN 119
QY 121 CCCAACAGCAGACCATTTTACTTCAGAGACTTCAGCCCTTTGAAGCAGCAGGTTTCAG 180
|||||
DB 120 PROASNPARGIHTHTLTHTLYRHPHEATGASPPHEATGPROLEUYSASPERRAPHEGIN 139
QY 181 CTGCTGAATTTTCTAGCAGTGAACCTCAAGTCACTGACGATGTCATTCATCTCGAT 240
|||||
DB 140 LEULEASNPHERSERSERERGLYULYSVALSERLEUTHRTASNALSERILIESERAP 159
QY 241 GAAGGAGATTACTTCTGCAGCTCTACAGCGACCCCAAGAGAGATTACACCACATC 300
|||||
DB 160 GUGLYARGTYRHPHCYSGIULEUTYRTHTASPPROGLINLSERTYTHRTHTTILE 179
QY 301 ACAGTCTGCTGCTCTCCAGCTAATCTGATGATGATGATGATGATGATGATGATGATGAT 360
|||||
DB 180 THTVALLEUVALPROPTHTHTASNPHEATGATLEASPDILEGLINYSPTHTALVALIGLU 199
QY 361 GGGAGAGATTTGAATCAAGTCAAGTGTACTGCCATGCGCAGACAGCCAGCAGCATCAG 420
|||||
DB 200 GILYUGIULILEGLUVALASNPCTHTHTALAMEALASERTLYSPROLAHTHTHTILEATG 219
QY 421 TGGTTCAAGGGAACCAAGCAACTCAAGGCAATATCAGAGTGAGAGATGTCGACATG 480
|||||
DB 220 TTPHLYGLYASNPILYSGIULEULYSGLYLSYSERTGLUVALIGLUITRPSERASPMEI 239
QY 481 TACACTGTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
|||||
DB 240 TYRTHVALTHSERLINLEUETLEULYSVALIHISLYSGIULASPAISPGIYALPROVAL 259
QY 541 ATCTGCGAGGTGAGACACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
|||||
DB 260 IIECYSGIULVALIHPROALVALIHTHGLYASNPGLINHTHTHTHTHTHTHTHTHTHT 279
QY 601 GTGCACTATAAACCGCAAGTCGATATCCAGATGACTTACCCTCTGCAAGCCCTAACCCGG 660
|||||
DB 280 VALGINTYLYSPROGLINVAIHSLIEGLIMETHTTYPROLEUCLINGLYEUTHRATG 299
QY 661 GAAGGGAGTCATTTGAGTTAAGCTGTGAAGCATTCGGGAAGCCCAAGCCTGTGATGTA 720
|||||
DB 300 GUGLYASPAIAPhEGLIUEUTHRCYSGIUALALEGLYLSYPROGLINPROVALMETVA 319
QY 721 ACTTGCGTGAGAGTCGATGATGAATGCTCTCAACATGCGCTACTGTCTGGCCAAACCTG 780
|||||
DB 320 THTTPVALATGVALASPAISPGIUMETCTROGLINHISALVALLEUSERLYPROKASNLEU 339
QY 781 TTCATCAATTAACCTTAACAAACAGATTAACGGTACTTACCCTGTGAGGCTTCCACATAT 840

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|||||
Db 340 PheIIeasmsnleuasnlysthrAspsnGLythrYrgrGcyluaISerAsnIle 359
QY 841 GTGGGAAGGCTCATTTGGGACTATATGCTGATGTATATGATATCCGCCACAACTATCCCT 900
Db 360 ValGLyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProPorphrThrIlePro 379
QY 901 CCTCCCAACAACACCACTACCACTACCAACACCACTACCTTACCATCATC 960
Db 380 ProPorphrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 399
QY 961 ACA-----GATTCTGAGCAGGTGAAGAGGG 987
Db 400 ThrAspThrThrAlaThrThrGluProAlaValHisAspSerArgAlaGlyGluGly 419
QY 988 ACCATTGGGCGAGTGACAC 1008
Db 420 ThrIleGLyAlaValaLaspHis 426

RESULT 4
Q9BY67 ID Q9BY67 PRELIMINARY; PRT; 442 AA.
AC Q9BY67;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nectin-like protein 2.
GN NEC12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin
RT superfamily. ";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132811; AAF69029.1; -.
DR InterPro: IPR003599; Iq.
DR InterPro: IPR003598; Iq_G2.
DR InterPro: IPR003600; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR Pfam; PF00477; Iq; 3.
DR SMART; SM00409; Iq; 3.
DR SMART; SM00408; IqG2; 3.
DR SMART; SM00410; Iq_Like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Alignment Scores:
Pred. No.: 5.21e-144 Length: 442
Score: 1738.00 Matches: 331
Percent Similarity: 99.11% Conservative: 2
Best Local Similarity: 98.51% Mismatches: 3
Query Match: 96.34% Indels: 0
Db: 4 Gaps: 0

US-09-778-187b-3_copy_62_1069 (1-1008) x Q9BY67 (1-442)
QY 1 ATGCCCAAGGATGGAGACAGATCTGTTACTTAAGAGAGTGACAGTATGAGACAGA 60
Db 39 IleProThrGLyAspGLyGlnAsnLeuPheThrLysAspValThrValIleGluGlyGln 58
QY 61 GTGGCAACCATCATGCTGCAAGGTCAATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 59 ValAlaThrIleSerCysGlnValaLaspHisSerAspSerValIleGlnLeuAsn 78
QY 121 CCCAAGCAGCAGACCATTTACTTTCAGGAGCTTCAGGCTTTGAAGACAGACAGTTTTCAG 180
Db 79 ProAsnArgGlnThrIleTyrPheArgAspPheArgProLeuLysAspSerArgPheGln 98
QY 181 CAGCTGAATTTTCTAGCAGTGAAGTCAAAAGTGTACTGACGACGAATGTCTCATCTCGAT 240

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Db 99 LeuLeuAsnPheSerSerSerGluLeuLysValSerLeuThrAsnValSerIleSerAsp 118
QY 241 GAAGGCGATACATTTCCCGAGCTCTACAGGACCCGCCACAGAGATTTACACACATC 300
Db 119 GluGLyArgTyrPheCysGlnLeuTyrThrAspProGlnGlnSerTyrThrIle 138
QY 301 ACAATCCCTGCTTCCCTCCACCTTAACCTGATGATGATTCAGAAAGACAGCGAGTTGA 360
Db 139 ThrValLeuValProProArgAsnLeuMetIleAspIleGlnArgAspThrAlaValGlu 158
QY 361 GGGAGAGAGATTGAAGTCAACTGACTGCTGAGCCAGCAGACCGACGACCATCAGG 420
Db 159 GlyGluGlnIleGlnValaLaspHisSerThrAlaMetAlaSerLysProAlaThrThrIleArg 178
QY 421 TGGTTCGAAGGAAACAAGAACCTCAAGGCAATTCAGAGTGGAGAGTGGTGGACATG 480
Db 179 TrpPheLysGLyAsnThrGluLeuLysGLyLysSerGluValaGluGluTyrPheSerAspMet 198
QY 481 TACACTGTGACAGTCACTGATGCTGAAGGTGCACAGAGGAGACAGCGGGTCCCGTG 540
Db 199 TyrThrValThrSerGlnLeuMetLeuLysValHisLysGlnAspArgValaProVal 218
QY 541 ATCTGCCAGGTGAGACACCTCGGTGCATCTGGAACCTGCAGACCGCTATTTAGAA 600
Db 219 IleCysGlnValaGlnHisProAlaValaThrGlyAsnLeuGlnThrGlnArgTyrLeuGln 238
QY 601 GTCCAGATTAACCGGACAGGACGATATCCAGATGATGATTAACCTTGAAGGCTTAACCCGG 660
Db 239 ValGlnTyrAspProGlnValaHisIleGlnMetThrTyrProLeuGlnGlyLeuThrArg 258
QY 661 GAAGGGATGCATTTGATGATTAACGTGTGAAGCCCATCGGAGCCGACCTGATGATGTA 720
Db 259 GluGLyAspAlaLeuGlnLeuTyrGlyGlnAlaIleGlyLysProGlnProValaMetVal 278
QY 721 ACTTGGGTGAGAGTCAATGATGAATGCTCAACATGCGGTACTGTCTGGGCCAAACCTG 780
Db 279 ThrTrpValaArgValaLaspArgLysMetProGlnHisAlaValaLeuSerGlyProAsnLeu 298
QY 781 TTCATCAATTAACCTTAACAACAACAGATTAACGATTAACCGGTGATGATGATTAACATTA 840
Db 299 PheIleAsnAsnLeuAsnLysThrAspAsnGLyThrTyrArgGlnLaspSerAsnIle 318
QY 841 GTGGGAAGGCTCATTCGAGCTATATGCTGATGATGATGATGATGATGATGATGATGATGAT 900
Db 319 ValGLyLysAlaHisSerAspTyrMetLeuTyrValTyrAspProPorphrThrIlePro 338
QY 901 CCTCCCAACAACACCACTACCACTACCACTACCACTACCACTACCTTACCATCATC 960
Db 339 ProPorphrThrThrThrThrThrThrThrThrThrThrThrThrThrThrIleIle 358
QY 961 ACAGATTCTGAGCAGGTGAAGAGGACCATTTGGGCGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1008
Db 359 ThrAspSerArgAlaGlyGluGlySerIleArgAlaValaLaspHis 374

RESULT 5
Q9D6E7 ID Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2900073606Rik protein.
GN IGSF4 OR 2900073606Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
MEDLINE=21083660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flatschman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuohi P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sasaki K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlisch S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013775; BAB2898.1; -.
DR MGD; MGI:189272; Igsf4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
SO SEQUENCE 336 AA; 37157 MW; FF887FAFAEFPF120 CRC64;

Alignment Scores:
Pred. No.: 9,64e-127 Length: 336
Score: 1541.00 Matches: 293
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.42% Indels: 0
DB: 11 Gaps: 0

US-09-778-187B-3_COPY_62_1069 (1-1008) x Q9D6E7 (1-336)

OY 1 ATCCACAGAGTGTAGAGAGAGATCTTTTAAAGAGAGTGTGATGAGAGAA 60
DB 42 ILEPOTHCGLYASPGIYGLNASNLEUPHERHLYSASVALTHVALLIEGLUGLIU 61
OY 61 GTGGAGACCATGAGTCCAGAGTCAATAGAGTGCAGACTGATCCAGCTCCAGAC 120
DB 62 VALAATHTHLESERCSGLNVALSNLYSSERASPSERVALILEGLINLEUASN 81
OY 121 CCCAAGAGCAGACCATTTACTTCCAGGAGCTTCCAGGAGTTCAG 180
DB 82 PROAHNARGGINTHTLIERPHEARGASPRHEARGPROLEULYSASPERARGHEGIN 101
OY 181 CTGTGATATTTTTCAGCAGTGAAGTCAAGTGCAGAGATGTCTCAATTCGAT 240
DB 102 LEULASNPHERSERSERGLULEULYSVALSERLEUTHASVALSERLIESERASP 121
OY 241 GAAGGAGATCTTCTGCCAGCTTACAGGAGCCGCCAGAGAGATGACCCAGCATC 300
DB 122 GUGUATATGTYRPHECYSGLNLEUTYRTHASPRPROPGINGLISERTYRTHRTILE 141
OY 301 ACAGTCTGCTTCCTCCAGTAACTTGATGATGATGATGATGATGATGATGATGAT 360
DB 142 THVALLEVALLEVALLEVALLEVALLEVALLEVALLEVALLEVALLEVALLEVAL 161
OY 361 GGGGAGAGATTTGAAGTCACTGTACTGCCATGGCCAGAGCCAGCAGCATCAGG 420
DB 162 GUGUGUGUUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUG 181
OY 421 TGGTTCAAGGAG 480
DB 182 TRPHEULYSGLYASNLYSGILULEULYSGLYLYSSERGLUVALGLUGLUGLUGLUGLUG 201

OY 481 TACAGTGTGACAGTACAGTGTGATGCTGAAGTGCACAAAGAGAGAGAGAGAGAGAG 540
DB 202 TYRTHVALTHRSERGLNLEUETLEULYSVALINILYSGLNAPSAPDLYVALPROVAL 221
OY 541 ATCTGCCAGGTGAGACACCCCTGGCTCACTGGGAACCTGCAGACCCAGGCTATGAGA 600
DB 222 ILECYSGINVALGLNINISPROLAVALTHRGLYASNLEGINTHGLNHTGYRLEUGLI 241
OY 601 GTGAGTATTAACCCSAGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 242 VALGINTYRGLYRPGGLNVALINISILEGLINMETHTYRPROLEUGLNGLYEULHRTG 261
OY 661 GAAGGAGATGATTTGAGTTAAGTGTGAAGCCATGCGAAGCCAGCCAGCTGTAGTGA 720
DB 262 GUGUASPARLAPHEGLULEULHTRCYSGULALAILIEGLYLYSRPGGLNPROVALMETVAL 281
OY 721 ACTTGGGTGAGAGTGCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 282 THTRVALATGVALASPRASPRGLMETRPGGLNLSALVALLEULSERGLYRPROASNLEU 301
OY 781 TTCATCATTAACSTTAACAAACAGATTAACGCTTACCCCTGTGAGGCTTCAACATA 840
DB 302 RHEILASNASNLYSNLYSTHRSASNSGLYRTHRGATGCGULVALSERASNILE 321
OY 841 GTGGAAAGGCTCATTCGAGATATGCTGTATGATAC 879
DB 322 VALGLYSLANLHISERASPRTYMETLEULYTYRVALTYR 334

RESULT 6

Q922H8 PRELIMINARY; PRT; 295 AA.

AC Q922H8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Necilin-like protein 2.
GN IGSF4 OR NECIL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N. A.
RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel cDNA encoding a member of immunosuperfamily.";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF061260; AAC67243.1; -.
DR MGD; MGI:189272; Igsf4.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00294; 4.Im. 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
SO SEQUENCE 295 AA; 32509 MW; 9DE9D86F6F6F488 CRC64;

Alignment Scores:

Pred. No.: 3.57e-97 Length: 295
Score: 1204.00 Matches: 227
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.74% Indels: 0
DB: 11 Gaps: 0

US-09-778-187B-3_COPY_62_1069 (1-1008) x Q922H8 (1-295)

OY 328 ATGATGATATTCAG 387
DB 1 METILASPILEGILNLYSASPRHVALVALGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUG 20

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QY 388 GCCATGGCCAGCAAGCCAGGACACCATCAGGTGGTTCAAGGAACAAGAACTCAAA 447
    |||||||
Db 21 AlamelalaserlyproalaThrThrIleArgTPrpPheylsglysnlysgluLeuLys 40
QY 448 GGCAAATCAGAGGTGGAGAGTGTGGACATATACACTGTGACCAAGTCAAGTGTCTG 507
    |||||||
Db 41 GlyLysSerGluValGluGlnUtrPserAspMetTyrThrValThrSerGlnLeuMetLeu 60
QY 508 AAGGTGCACAAGAGGAGCAGCGGGGTCCGGTATCGCCAGGTGGAGGACCCCTGGCGTC 567
    |||||||
Db 61 LysValHisLysGlnUtrspbspglyValProValIleCysGlnValGlnHisProAlaVal 80
QY 568 ACTGGAACCTGCAGACCCAGCGCTATCTAGAAGTCAGATATAACCCAGTGCATATC 627
    |||||||
Db 81 ThrGlyAsnLeuGlnThrGlnArgTyrLeuGlnValGlnTyrLysProGlnValHisIle 100
QY 628 CAGATACACTACCCCTGCAGAGCCCTAACCCGGGAAGGGGATCATTTGAGTTAACTGT 667
    |||||||
Db 101 GlnMetThrTyrProLeuGlnGlyLeuThrArgGluGlyAspAlaPheGlnLeuThrCys 120
QY 688 GAAGCCATGGGAAGCCCAAGCCTGTGATGTAACTTGGGTGAGTGCATGTGAATG 747
    |||||||
Db 121 GluAlaIleGlyLysProGlnProValMetValThrTyrValArgValAspAspgluMet 140
QY 748 CCTCAACATGCGCTACTGTCTGGGCAAACTGTTTCATCATTAACCTAAACAAACAGAT 807
    |||||||
Db 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnAsnLeuAsnLysThrAsp 160
QY 808 AACGGTACTTACCGCTGTAGGGTCCCAACATATAGTGGAAAGGCTCATTCGACTATAG 867
    |||||||
Db 161 AsnGlyThrTyrArgCysGlnAlaSerAsnIleValGlyLysAlaHisSerAspTyrMet 180
QY 868 CTGTATGTATAGATCCCCCAACATATCCCTCTCCCAACAACACCAACCACTATAC 927
    |||||||
Db 181 LeuTyrValTyrAspProPheThrThrIleProPheThrThrThrThrThrThrThr 200
QY 928 ACCACCACCAACCAACCACTCTTACCATCATCAGATTCCTGCAGAGTGAAGGGG 987
    |||||||
Db 201 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 220
QY 988 ACCATTGGGGGAGTGGACCAC 1008
    |||||||
Db 221 ThrIleGlyAlaValAspHis 227

RESULT 7
O90YL4 PRELIMINARY: PRT: 306 AA.
AC O90YL4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RAI175C.
GN IGSP4 OR RAI175C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
RA Momoi T.;
RT "RAI75, a novel neuron specific adhesion protein.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021966; BAA67916.1; -.
DR MGD; MGI:1889272; IGsf4.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003600; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; ig_2.
DR IGsf4 OR RAI175A.
DR SMART; SM00294; 4.Im; 1.
DR SMART; SM00408; IGc2; 1.

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DR SMART; SM00410; IG_c1like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 306 AA; 33522 MW; AACB37B0F2354D5 CRC64;

Alignment Scores:
Pred. No.: 2,56e-94 Length: 306
Score: 1171.50 Matches: 224
Percent Similarity: 94.54% Conservative: 1
Best Local Similarity: 94.12% Mismatches: 2
Query Match: 64.94% Indels: 11
DB: 11 Gaps: 1

US-09-778-187b-3_copy_62_1069 (1-1008) x O90YL4 (1-306)
QY 328 ATGATGATATATCCAGAAAGACAGCGAGTTGAAGGGAGAGATTGAATCACTACT 387
    |||||||
Db 1 MetIleAspIleGlnLysAspThrAlaValGlnGlyGlnGlnIleGlnValAsnGlyThr 20
QY 388 GCCATGGCCAGCAAGCCAGCAGCAGCATCAGGTGGTTCAAGGAACAAGAACTCAAA 447
    |||||||
Db 21 AlamelalaserlyproalaThrThrIleArgTPrpPheylsglysnlysgluLeuLys 40
QY 448 GGCAAATCAGAGGTGGAGAGTGTGGACATATACACTGTGACCAAGTCAAGTGTCTG 507
    |||||||
Db 41 GlyLysSerGluValGluGlnUtrPserAspMetTyrThrValThrSerGlnLeuMetLeu 60
QY 508 AAGGTGCACAAGAGGAGCAGCGGGTCCGGTATCGCCAGGTGGAGCAGCCTGGCGTC 567
    |||||||
Db 61 LysValHisLysGlnUtrspbspglyValProValIleCysGlnValGlnHisProAlaVal 80
QY 568 ACTGGAACCTGCAGACCCAGCGCTATCTAGAAGTCAGATATAACCCAGTGCATATC 627
    |||||||
Db 81 ThrGlyAsnLeuGlnThrGlnArgTyrLeuGlnValGlnTyrLysProGlnValHisIle 100
QY 628 CAGATACACTACCCCTGCAGAGCCCTAACCCGGGAAGGGGATCATTTGAGTTAACTGT 667
    |||||||
Db 101 GlnMetThrTyrProLeuGlnGlyLeuThrArgGluGlyAspAlaLeuGlnLeuThrCys 120
QY 928 ACCACCACCAACCAACCACTCTTACCATCATCAGATTCCTGCAGAGTGAAGGGG 987
    |||||||
Db 121 GluAlaIleGlyLysProGlnProValMetValThrTyrValArgValAspAspgluMet 140
QY 748 CCTCAACATGCGCTACTGTCTGGGCAAACTGTTTCATCATTAACCTAAACAAACAGAT 807
    |||||||
Db 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnAsnLeuAsnLysThrAsp 160
QY 808 AACGGTACTTACCGCTGTAGGGTCCCAACATATAGTGGAAAGGCTCATTCGACTATAG 867
    |||||||
Db 161 AsnGlyThrTyrProCysGlnAlaSerAsnIleValGlyLysAlaHisSerAspTyrIle 180
QY 868 CTGTATGTATAGATCCCCCAACATATCCCTCTCCCAACAACACCAACCACTATAC 927
    |||||||
Db 181 LeuTyrValTyrAspProPheThrThrIleProPheThrThrThrThrThrThrThr 200
QY 928 ACCACCACCAACCAACCACTCTTACCATCATCAGATTCCTGCAGAGTGAAGGGG 987
    |||||||
Db 201 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 220
QY 964 -----GATTCGAGCAGGTGAAGAGGGAGCATTTGGGCGAGTGGACAC 1008
    |||||||
Db 221 AlaValHisAspSerArgAlaGlyGlnGlnGlyThrThrIleGlyAlaValAspHis 238

RESULT 8
O90YL6 PRELIMINARY: PRT: 295 AA.
AC O90YL6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RAI175A.
GN IGsf4 OR RAI175A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kuroku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein";
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB021964; BAA87914.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR InterPro; IPR003598; IG-C2.
 DR InterPro; IPR003600; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.Im; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00410; IG-like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA: 32347 MW: FDD9E8145C689718 CRC64:

Alignment Scores:
 Pred. No.: 1.6e-92 Length: 295
 Score: 1151.00 Matches: 217
 Percent Similarity: 96.48% Conservative: 2
 Best Local Similarity: 95.58% Mismatches: 8
 Query Match: 63.80% Indels: 0
 DB: 11 Gaps: 0

US-09-778-187b-3_COPY_62_1069 (1-1008) x 090YL6 (1-295)

OY 328 ATGATCGATATTCAGAAACACACGCGAGTTGAAGGGAGAGATTGAAGTCAACTACT 387
 DB 1 MettIleAspIleGlnLysAspThrAlaValGluGluGluIleGluValAsnCysThr 20
 OY 388 GCCATGCCAGCAGCAGCAGCAGCAGCAGCAGTGTGTTCAAGGGAGAAAGCAACTCAAA 447
 DB 21 AlameAlaSerLysProAlaThrThrIleArgTTPRphelGlyAsnLysGluLeuLys 40
 OY 448 GGCAAATCAGAGGTGAGAGAGTGTGCGACATGTACACTGTGACAGTCAGTGTATG 507
 DB 41 GlyLysSerGluValGluIuTrpSerAspMetTyrThrValThrSerGlnLeuMetLeu 60
 OY 508 AAGGTGCACAAAGAGAGACACGCGGTCCGGTGATGTGCCAGGTGGAGACACCTGGGGTC 567
 DB 61 LysValIleHisLysGlnAspAspGlyValProValIleCysGlnValGluIleAspProAlaVal 80
 OY 568 ACTGGAACCTCAGACCCAGCGCTATAGAAAGTGCATATTAACCGCAAGGCATATC 627
 DB 81 ThrGlyAsnLeuGlnThrGlnArgTyrLeuGluValGlnTyrLysProGlnValHisIle 100
 OY 628 CAGATGACTTACCTCTGCAAGGCTTAACCGGGAAGGGAGATGATTTGAAGTGT 687
 DB 101 GlnMetThrTyrProLeuGlnGlyLeuThrArgGluGlyAspAlaLeuGluLeuThrCys 120
 OY 688 GAAGCATCGGGAAGCCCGAGCTGTGATGTACTGGGTGAGAGTCATGTGAATG 747
 DB 121 GlnAlaIleGlyLysProGlnProValIleThrTyrValArgValAspAspGluMet 140
 OY 748 CCTCAACATGCGGTACTGTGGGCCAAACGTTTCATCAATTAACCTTAACAACAGAT 807
 DB 141 ProGlnHisAlaValLeuSerGlyProAsnLeuPheIleAsnHisLeuAsnLysThrAsp 160
 OY 808 AACGCTACTTACCGCTGTAGAGCTTCAACATAGTGGAAAGGCTCATTCGAGCTATAG 867
 DB 161 AsnGlyThrTyrProCysGlnAlaSerAsnIleValGlyLysAlaHisSerAspTyrIle 180
 OY 868 CTGTATGTATACGATCCCGCCACAACTATCCTCTCCACAAACACACACCACTACC 927
 DB 181 LeuTyrValIlyAspProThrThrIleProProThrThrThrThrThrThrThr 200
 OY 928 ACCACACACACACACACCTCTTACCATCATCACAGATTCTCGACAGTGAAGGGGG 987
 ||||||||||| ||| :||| ||||||||||| |||||||||||

DB 201 ThrThrThrThrAlaThrThrGluProAlaValHisAspSerArgAlaGlyGluGly 220
 OY 988 ACCATTGGGGCAGTGGACCAC 1008
 DB 221 ThrIleGlyAlaValAspHis 227

RESULT 9

O90YL5 ID O90YL5 PRELIMINARY: PRT: 289 AA.
 AC O90YL5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Adhesion protein RA175B.
 GN Igsf4 OR RA175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kuroku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein";
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB021965; BAA87915.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR InterPro; IPR003598; IG-C2.
 DR InterPro; IPR003600; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.Im; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00410; IG-like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 289 AA: 31811 MW: 8D1B836D0565A8E4 CRC64:

Alignment Scores:
 Pred. No.: 1.04e-84 Length: 289
 Score: 1062.00 Matches: 205
 Percent Similarity: 91.19% Conservative: 2
 Best Local Similarity: 90.31% Mismatches: 14
 Query Match: 58.87% Indels: 6
 DB: 11 Gaps: 1

US-09-778-187b-3_COPY_62_1069 (1-1008) x 090YL5 (1-289)

OY 328 ATGATCGATATTCAGAAACACACGCGAGTTGAAGGGAGAGATTGAAGTCAACTACT 387
 DB 1 MettIleAspIleGlnLysAspThrAlaValGluGluGluIleGluValAsnCysThr 20
 OY 388 GCCATGCCAGCAGCAGCAGCAGCAGCAGTGTGTTCAAGGGAGAAAGCAACTCAAA 447
 DB 21 AlameAlaSerLysProAlaThrThrIleArgTTPRphelGlyAsnLysGluLeuLys 40
 OY 448 GGCAAATCAGAGGTGAGAGAGTGTGCGACATGTACACTGTGACAGTCAGTGTATG 507
 DB 41 GlyLysSerGluValGluIuTrpSerAspMetTyrThrValThrSerGlnLeuMetLeu 60
 OY 508 AAGGTGCACAAAGAGAGACACGCGGTCCGGTGATGTGCCAGGTGGAGACACCTGGGGTC 567
 DB 61 LysValIleHisLysGlnAspAspGlyValProValIleCysGlnValGluIleAspProAlaVal 80
 OY 568 ACTGGAACCTCAGACCCAGCGCTATAGAAAGTGCATATTAACCGCAAGGCATATC 627
 DB 81 ThrGlyAsnLeuGlnThrGlnArgTyrLeuGluValGlnTyrLysProGlnValHisIle 100
 OY 628 CAGATGACTTACCTCTGCAAGGCTTAACCGGGAAGGGAGATGATTTGAAGTGT 687
 DB 101 GlnMetThrTyrProLeuGlnGlyLeuThrArgGluGlyAspAlaLeuGluLeuThrCys 120
 OY 688 GAAGCATCGGGAAGCCCGAGCTGTGATGTACTGGGTGAGAGTCATGTGAATG 747
 ||||||||||| ||| :||| ||||||||||| |||||||||||

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Db 121 G1uAla1leG1ySPROGInPrOvalMeCValThrTrpValArgValaSPaSPG1umEt 140
QY 748 CcTCAACATCCGCTACTGTCGTGGGCCAAACCTGTCATCAATTAACCAAAACAAGCAT 807
Db 141 ProGlnH1sAlaValLeuSerGlyProAsnLeuPhe1leAsnLnLeuAsnLysThrAsp 160
QY 808 AACGGTACTTACCGCTGTGAGGCTTCCACATAGTGGAAGGCTCATTCGAGCTATATG 867
Db 161 AsnGlyThrTrpProcysGluAlaSerAsn1leValGlyLysAlaHisSerAspTyrIle 180
QY 868 CcTATATGTATACATGCCCCCAACATATGCCCTCCCTCCCAACAACACCACCACCTACC 927
Db 181 LeuTyrValIyrAspThrThrThrThrIle-----LeuThrIleIle 194
QY 928 ACCACACACACACACATCTTACCATCATCAGATTCCTGAGCAGGTGAAGAGGG 987
Db 195 ThrAspThrThrAlaThrThrGluProAlaValAlaHisAspSerArgAlaGlyGluGly 214
QY 988 ACCATTGGGGCAGTGACAC 1008
Db 215 ThrIleGlyAlaValaSPaSPHs 221

```

RESULT 10

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QY0YL3 PRELIMINARY; PRT; 278 AA.
AC QY0YL3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RAI15N.
GN IGSF4 OR RAI15N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kuroku Y., Momoi M.,
RA Momoi T.;
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021967; BAA87917.1; -.
DR MGD; MGI:1889272; Igsf4.
DR InterPro: IPR003598; Iq_C2.
DR InterPro: IPR003600; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003585; Neutxin-Like.
DR Pfam; PF00047; Iq_2.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00410; Igc_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;

```

Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 1.19e-82	278	200
Percent Similarity: 1038.50		200
Best Local Similarity: 88.99%		2
Query Match: 57.57%		17
DB: 11	Gaps:	1

US-09-778-187b-3_copy_62_1069 (1-1008) x QY0YL3 (1-278)

```

QY 328 ATGATGATATCCAGAAACACGCGAGTTGAAGGAGAGATTTGAAGTCAACTGACT 387
Db 1 MetIleAspIleGlnLysAspThrAlaValAlaGluGlyGluGluIleGluValaSPaSPHs 20
QY 388 GCCATGGCAGACGACGACGACGACGACGATTCAGTGGTTCAAAGGGAACGAACTCAAA 447
Db 21 AlaMetAlaSerLysProAlaThrThrIleArgTTrpPheLysGlyAsnLysGluLeuLys 40

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QY 448 GGCAAATCAGAGGTGGAGAGGTGGAGATGTACATGTGACAGTCACTGATGCTG 507
Db 41 GlyLysSerGlnValAlaGluGluTTrpSerAspMetGlyThrValThrSerGlnLeuMetLeu 60
QY 508 AAGGTGCACAGAGGAGACGAGCGGGTCCCGGTATCTGCCAGGTGGAGACCTCGGGTTC 567
Db 61 LysValHisLysGlnAspAspGlyValProValIleLysGlnValAlaGluHisProAlaVal 80
QY 568 ACTGAAACCTGCAGACCCAGCGCTATCTGAGATGCAGATATTAACCGCAAGTATATC 627
Db 81 ThrGlyAsnLeuThrThrGlnArgTyrLeuGlnValAlaGlnTyrLysProGlnValHisIle 100
QY 628 CAGATGACTTACCTCTGTGCAAGGCTTAACCGGGAAGGAGTCAATTTGAGTTAAGTGT 687
Db 101 GlnMetThrTyrProLeuGlnGlyLeuThrArgGlyGlyAspAlaLeuGlnLeuThrCys 120
QY 688 GAAGCCATCGGGAAGCCCGCTGTGATGTGTAATTTGGGTGAGATCGATGTATGAATG 747
Db 121 G1uAla1leG1ySPROGInPrOvalMeCValThrTrpValArgValaSPaSPG1umEt 140
QY 748 CcTCAACATCCGCTACTGTCGTGGGCCAAACCTGTCATCAATTAACCAAAACAAGCAT 807
Db 141 ProGlnH1sAlaValLeuSerGlyProAsnLeuPhe1leAsnLnLeuAsnLysThrAsp 160
QY 808 AACGGTACTTACCGCTGTGAGGCTTCCACATAGTGGAAGGCTCATTCGAGCTATATG 867
Db 161 AsnGlyThrTrpProcysGluAlaSerAsn1leValGlyLysAlaHisSerAspTyrIle 180
QY 868 CcTATATGTATACATGCCCCCAACATATGCCCTCCCTCCCAACAACACCACCACCTACC 927
Db 181 LeuTyrValIyrAsp----- 185
QY 928 ACCACACACACACACATCTTACCATCATCAGATTCCTGAGCAGGTGAAGAGGG 987
Db 186 -----ThrThrAlaThrThrGluProAlaValAlaHisAspSerArgAlaGlyGluGly 203
QY 988 ACCATTGGGGCAGTGACAC 1008
Db 204 ThrIleGlyAlaValaSPaSPHs 210

```

RESULT 11

```

QY0R464 PRELIMINARY; PRT; 388 AA.
AC QY0R464:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Membrane glycoprotein.
GN TSL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Fukami T., Maruyama T., Murakami Y.;
RT Identification of a murine ortholog of the TSLC1-like gene 2.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059394; AAL29692.1; -.
KW NCBI_TaxID=10090;
SQ SEQUENCE 388 AA; 42723 MW; 8E3A9DF1C3B9D23E CRC64;

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Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 3.08e-46	388	123
Percent Similarity: 624.00		123
Best Local Similarity: 61.06%		62
Query Match: 40.59%		112
DB: 11	Gaps:	6
		3

US-09-778-187b-3_copy_62_1069 (1-1008) x QY0R464 (1-388)

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QY 10 GGTGATGACAGAAATCTGTTACTAAAGACGTGACAGTGTGAAGAGAGAGTGCACACC 69

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Db 161 ThValAlrPhearGyValAspArgLyAspAspGlyLeilelleCysGlnAlaGln 180
QY 556 CACCTGCGGCTGACTGGA-----AACCTGCAGACCCAGCGCTATAGAGTGCAGTAT 609
QY 181 AsnGlnAlaLeuProSerGlyHisSerLysGlnThrGlnValLeuAspValGlnTyr 200
QY 610 AAACCCGAAGTGCATATCCAGATGACTTACCCTCTGCAGAGCCTAACCCGGGAGGAGAT 669
Db 201 SerProThrAlaArgLeuHisAlaSer-----GlnAlaValAlaArgGlnGlyAsp 217
QY 670 GCATTTAGTTAGTAAAGCTGGAAGCCAGCCAGCTGTAGTAACTTGGGTG 729
Db 218 ThrLeuValLeuThrCysAlaValThrGlyAsnProArgProAsnGlnIleArgTyrAsn 237
QY 730 AGAGTCGATGATGAAATGCTCAACATCCGCTACTGTCTGGCCAACTGTTCAAT 789
Db 238 ArgGlyAsnGlnSerLeuProGlnArgAlaGlnAlaValGlyGlnThrLeuThrLeuPro 257
QY 790 AACCTAAACAACACATTAACGCTACTTACCCTGTGAGCCTTCCAAATAGTGGGAAAG 849
Db 258 GlyLeuValSerAlaAspAsnGlyThrTyrThrCysGlnAlaSerAsnLysHisGlyHis 277
QY 850 GCATATCGCATATATAGCTGTATGATAGATCCC-----CCCAACACT--- 894
Db 278 AlaArgAlaLeuThrValLeuValValTyrGlyGlnSerArgLeuArgProThrGlnGly 297
QY 895 -----ATCCCTCTCCCAACACACACACACACACACACACACACACACACAC 945
Db 298 GlyGlyGlyAlaProAspProGlyAlaValAlaGlnAlaGlnThrSerValProTyrAla 317
QY 946 ATCCTT 951
Db 318 IleVal 319

RESULT 13
099N28
ID 099N28 PRELIMINARY; PRT; 396 AA.
AC 099N28;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein).
GN NECT1 OR TSL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RT "Cloning and expression analysis of novel mouse cDNA encoding a
RT membrane protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of a murine ortholog of the TSLC1-like gene 1.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF195662; AAC35584.1; -;
DR EMBL: AY059393; AAL28691.1; -;
DR MGI: 2137858; Nect1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_3.
DR SMART: SM00408; IgC2_3.
DR SMART: SM00410; IG_Like_2.
KW Immunoglobulin domain.
SEQUENCE 396 AA; 42964 MW; C1ADF8B57D141F3A CRC64;

Alignment Scores:
Pred. No.: 1, 22e-33 Length: 396
Score: 480.50 Matches: 109
Percent Similarity: 55.63% Conservative: 64
Best Local Similarity: 35.05% Mismatches: 119
Query Match: 26,64% Indels: 19
DB: 11 Gaps: 7

US-09-778-187b-3_copy_62_1069 (1-1008) x 099N28 (1-396)

QY 13 GATGACAGATATCTGTTACTAAAGCAGTACAGTATTAAGAGAGAGTGCACATC 72
Db 27 AspAspSerGlnProThrThrSerAspGlnThrValValAlaGlyThrValValLeu 46
QY 73 AGCTGCAGGCTCATATAAGATGACAGTACAGTACAGTACAGTACAGTACAGTACAG 132
Db 47 LysCysGlnValValLysAspHisGlnAspSerLeuGlnThrSerAsnProAlaGlnGln 66
QY 133 ACCATTTACTTCAAGGAGCTTCAAGCCTTTGAGAGACAGCAGTTTCACTGTGAATT 192
Db 67 ThrLeuThrPhelGlyGlnLysArgAlaLeuArgAspAsnArgIleGlnLeuValSerSer 86
QY 193 TCTAGCAGTAACTCAAAAGTCACTGACGACGACGACGACGACGACGACGACGACG 252
Db 87 ThrProHisGlnLeuSerLeuSerLeuSerLeuSerValAlaLeuAlaAspGlnGlyTyr 106
QY 253 TTCTGCAGGCTTCAAGGAGCTTCAAGCCTTTGAGAGAGTATACACATCACTGTGTT 312
Db 107 ThrCysSerIlePhelThrMetProValArgThrAlaLysSerLeuValThrValLeuGly 126
QY 313 CCTTCACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 372
Db 127 IleProGlnLysProIleThrIleThrGlyTyrLysSerSerLeuArgGlnLysGlnAla 146
QY 373 GAAGTCACTGACTGCTGACGACGACGACGACGACGACGACGACGACGACGACGAC 432
Db 147 ThrLeuAsnGlnSerLeuSerGlySerProAlaGlnAlaGlnThrThrPargLysGly 166
QY 433 AACAGGAAGTCAAAAGC---AAATCAGAGGTGAGAGAGTGGCGAC-----ATGTAC 483
Db 167 AspGlnGlnLeuLeuHisGlnLysAspGlnThrArgIleGlnGlnAspProAsnGlyThrPhe 186
QY 484 ACTGTGACAGTCACTGATGCTGAAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAG 543
Db 187 ThrValSerSerSerValSerPheGlnValThrArgGlnAspAspGlyAlaAsnIleVal 206
QY 544 TGCCAGGTGAGAGACCCCTGGGTCACTGGA---AACCTGAGACCCAGCGCTTCTAGAA 600
Db 207 CysSerValAsnHisGlnSerLeuLysGlyAlaAspArgSerThrSerGlnArgIleGln 226
QY 601 GTTCAGTATTAACCGCAAGTGCATATCCAGATGACTTACCCTCTGCAAGGCTAACCCGG 660
Db 227 ValLeuTyrThrProThrAlaMetIleArg-----ProGlnProAlaHisProArg 243
QY 661 GAAGGAGATGATTTAGTTAACTGTGAAGCCATCGGAGAGCCCAAGCCTGTGATGTA 720
Db 244 GlnGlyGlnLysLeuLeuLeuHisCysGlnGlyArgGlyAsnProValProGlnGlnTyr 263
QY 721 ACTGGGTGAGAGTCAATGATAATGCT-----CAAAATCCCGTACTGTCT 768
Db 264 ValThrValLysGlnGlySerGlnProProLeuLysMetThrGlnLeuAlaLeuIle 283
QY 769 GGGCCAAACCTGTTTCATATACTAAACAACAGATTAACGCTACTTACCGCTGTGAG 828
Db 284 PhePro-----PheLeuAsnLysSerAspSerGlyThrTyrGlyCysThr 298
QY 829 GCTTCAACATAGTGGAAAGGCTCAATTCGGACTATATCTGTATGATACATCCGCC 888
Db 299 AlaThrSerAsnMetGlySerTyrThrAlaTyrPheThrLeuAsnValAsnAspProSer 318
QY 889 ACACTATCCCTCTCCCAACACACACACACACACACACACACACACACACACACAC 921
Db 319 -----ProValProSerSerSerSerThr 326

RL Nature 409:685-690(2001).
 DR EMUL, AK0119449: BAB37933.1. -
 DR MGD, MGI:1914402:2610301B19RLK.
 DR InterPro, IPR003599: Ig.
 DR InterPro, IPR003600: Ig_1like.
 DR InterPro, IPR003006: Ig_MHC.
 DR Pfam: PF00047, Ig: 2.
 DR SMART, SMO0409: IG_1.
 DR SMART, SMO0410: IG_1like_1.
 SQ SEQUENCE 549 AA: 60703 MW: 32775C5BEC7319B32 CRC64:

Alignment Scores:

Pred. No.:	136e-17	Length:	549
Score:	298.00	Matches:	93
Percent Similarity:	44.01%	Conservative:	65
Best Local Similarity:	25.91%	Mismatches:	159
Query Match:	16.52%	Indels:	42
DB:	11	Gaps:	11

US-09-778-187B-3_COPY_62_1069 (1-1008) x Q9D006 (1-549)

16 GGACAGAATCTGTTACTAAAGACGTGACAGTGATTGAAGGAGAAGTGGCAACCATCAGC 75

Db 58 GlyceriIleIleValGluProHisValThrAlaValTyrPcGlyLysAsnValSerLeuLys 77

[illegible]

18 Cysleuallleuallashnclunlllellnglnlleseetrrglululslllenlsclululs 9/

27 124 ATCAGGCGACCAI TACTTCAGGACTTCAGGCCITGAG 16
 ::: |||||::: || :::
 ::: |||||::: || :::

22 20 OCT 1963 1111 VAIRDAVAIRNISHIFLOOINII YIOIYNESEI VAIGIINIGLYASPIYI 11

[illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

[illegible][illegible]

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      ::||| ||||:::||||| |
150 AjaCnCoCcCbmbvayl rvyo]c]:DmEb-vyrlG-uy}~
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[illegible]

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177 G]vproasnsersert]ebenc]wclwascn]uthtv]a]a]a]a]v]a]c]w]v]a]c]o]r]e]c]e]x 10
|||:::~::~|||  |||  ::|  |||  :::

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394 GCCAGCAAGCCAGCGAGCACCATCAGGTGTTCAAAAGGGAACCAAGGAATCCTAAAGGCCAA 45

Db 197 ThrGlyLysProValAlaGlnIleAspTrp---GluGlyAspLeuGlyGlyIleArgGlyIlePhe 21

QY 454 TCAGAGGTGAGGAGTGGTCCGACATGTACACTGTGACCAGTCAGCTGATGCTGAAGGTG 51

Db 216 SerThrIleSerPheLeuAsnGluThrAlaThrIleValSerGlnTYrGluLeuPhePro 23

QY 514 CACAAGGAGGACGACGGGTCCTCGGTGATCTGCCAGGTGGAGCACCTGCGGTCACTGA 57

Db 236 ThrArgPheAlaArgGlyArgArgIleThrCysValValLysHisProAlaLeuGluLys 25

574 AACCTGCAGACCCAGCGCTATCTAGAGTGCAGTATAAACCGCAAGTGCATATCCAGATG 63

Db 256 AspIleArgTyrSerPheIleLeuAspIleGlnTyrAlaProGluValSerValThrGly 27

634 ACTTACCCTCTGCAAGGCTAACCCGGGAAGGGATGCATTGAGTTAACGTGTGAAGCC 69

Db 276 TYRASPGLYASNTTPHVEALGLYARGLYGly-----VALASNLEULYSCYSASNAIa 29

694 ATCGGGAAGCCCCAGCCTGTGATGGTAAGTGGGTGAGAGTCGATGATGAATGCCCTCAA 75

DB 294 ASPALGASINPROPHLYSSERVALTRPSEARGLLEUASPCLYGINTRPROASP 31

QY	754	CAIGCCGTAAGTGTCTGGGGCCAAACCTG---TTCATTCATAATACCAACCAACAGATATAC	81.0
		:::	:::
Db	314	GlyIeuLeuIaIaSerAspAsnThrLeuHisValHisProIeuThrValAsnTyrSer	333
QY	811	GSTACTACCGCTGTGAGGCTTCACATAAGTGGAAAGGCTCATTCGGACTATATGCTG	87.0
			:::
Db	334	GlyValTyrValCysLysValSerAsnSerLeuGlyIaIaSerAspIaIaSerValIle	353
QY	871	TATGTAATACGATGCCCTCC---ACAACTATGCCCTCT-----	903
		: :	
Db	354	TyrIleSerAspProIofThrThrThrLeuGlnProThrValGlnTPrHisSer	373
QY	904	-----CCCAACAACACCCACC	921
Db	374	ProIaIaSerValGlnAspIleAlaThrGlnHisLysLysIeuProPheProIeuSerThr	393
QY	922	ACTACACACACACACACACATCTTCATTCATTCACAGATTTCGACGAGGT	978
Db	394	LeuAlaThrIeuLysAspAspThrIleGlyThrIleIleAlaSerValGlyGly	412

Search completed: November 20, 2002, 07:56:07
Job time : 77.25 secs

Job time : 77.25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 ; Search time 12.5 Seconds
(without alignments)
790,888 Million cell updates/sec

Title: US-09-778-187b-4_COPY_21_356

Perfect score: 1765

Sequence: 1 IPTDGGONLFTKDYVIEGE.....LTIITDSRAGEGTIGAVDH 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

262574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625.5	35.4	421	2	US-08-659-984A-1
2	625.5	35.4	421	4	US-08-659-984A-1
3	625.5	35.4	444	2	US-08-659-984A-5
4	625.5	35.4	444	4	US-08-659-984A-5
5	231	13.1	393	1	US-08-429-742-2
6	204.5	11.6	388	1	US-08-429-742-4
7	204.5	11.6	458	4	US-09-435-956A-1
8	204	11.6	642	1	US-08-217-299-1
9	204	11.6	698	2	US-08-602-725-36
10	204	11.6	734	2	US-08-389-459A-17
11	204	11.6	734	3	US-08-987-867A-17
12	193	10.9	1395	4	US-09-540-245A-15
13	192	10.9	1651	4	US-09-540-245A-18
14	191.5	10.8	583	2	US-08-433-016-2
15	191.5	10.8	583	2	US-08-684-594-2
16	187.5	10.6	325	2	US-08-414-657D-6
17	187.5	10.6	325	2	US-08-414-657D-2
18	187.5	10.6	325	2	US-08-414-657D-41
19	187.5	10.6	325	4	US-09-135-080-2
20	187	10.6	287	2	US-08-414-657D-48
21	187	10.6	304	2	US-08-414-657D-44
22	185.5	10.5	315	2	US-08-414-657D-47
23	185.5	10.5	338	2	US-08-414-657D-42
24	185.5	10.5	338	2	US-08-414-657D-43
25	185.5	10.5	338	4	US-09-135-080-4
26	185.5	10.5	1241	4	US-09-040-774-2
27	185	10.5	287	2	US-08-414-657D-49

28	185	10.5	310	2	US-08-414-657D-45	Sequence 45, Appl
29	183.5	10.4	477	2	US-08-432-016-3	Sequence 3, Appl1
30	183.5	10.4	477	2	US-08-684-594-3	Sequence 3, Appl1
31	183.5	10.4	1297	4	US-09-540-245A-17	Sequence 17, Appl
32	179.5	10.2	338	2	US-08-414-657D-60	Sequence 60, Appl
33	179.5	10.2	338	4	US-09-135-080-8	Sequence 8, Appl1
34	177	10.0	1447	4	US-09-041-886-25	Sequence 25, Appl1
35	177	10.0	1447	5	PCT-US94-05277-2	Sequence 2, Appl1
36	174.5	9.9	478	5	PCT-US95-08493-15	Sequence 15, Appl
37	174.5	9.9	860	5	PCT-US95-08493-19	Sequence 19, Appl
38	174.5	9.9	868	5	PCT-US95-08493-21	Sequence 21, Appl
39	173.5	9.8	408	4	US-09-724-864-62	Sequence 62, Appl
40	172.5	9.8	869	1	US-08-374-834-16	Sequence 16, Appl
41	172.5	9.8	869	2	US-08-644-871-29	Sequence 29, Appl
42	172.5	9.8	869	4	US-09-077-955-33	Sequence 33, Appl
43	172	9.7	607	2	US-08-752-307B-12	Sequence 12, Appl
44	172	9.7	607	4	US-09-707-802-12	Sequence 12, Appl
45	172	9.7	607	4	US-09-991-326-12	Sequence 12, Appl

ALIGNMENTS

```

RESULT 1
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
;
GENERAL INFORMATION:
;
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1
Query Match 35.4%; Score 625.5; DB 2; Length 421;
Best Local Similarity 39.0%; Pred. No. 1.2e-47;
Matches 137; Conservative 66; Mismatches 121; Indels 27; Gaps 6;

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	Matches	137;	Conservative	66;	Mismatches	121;	Indels	27;	Gaps	6
QY	6	GONLFTKDYVTEGEVATITSCOVNKSDDSVIOLLNPNOTITTFRDFRPLKDSRFOLLNS	65							
Db	10	GGPFLITONVTEGGTALITTCRVDDNDNTSLQMSNPAQOTLTFDDKALKARDNRIETLVSAS	69							
QY	66	SEELVSLTNVSIISDEGRFCOLYDDPDESVTITVLEPPNMLMDIKDQNAVEGEETE	125							
Db	70	WHELISVSDVSLSEGGOTCSLTFMPKATSAVLTIVLGVPERKPOLSGFSSPYMBESDLMQ	129							
QY	126	VNCSTMAKRPATPIIMFPGNKELKJCKSEVEENS---DMYTSQLMLKHNKEDDGVYIC	182							
Db	130	LTCIKSSGSKPADIDIMFKNDKEIKQVYKYLAKEDARNKPTTVESTIDFRDRSDDDGAVIIC	189							
QY	183	QVEHPAVTGNLQ--TQRYLEVOYKKPOVNIQMTYPLQGLTREGDAFELTCEAIKPPQPMVT	241							
Db	190	RVDHESLNAIPQVAMQVLEIHTYPSVKI---IPSTPPQEGPILITTCESKSKPLPEPVL	246							
QY	242	WVRVUDDEN--PQHAVLSGPNLFINMLKNTDNGTYRCEASNIYVGKASHDMLVYDPPITI	299							
Db	247	WTKDGELPDDPRMVAVSGEHLILFLNKNDNGTYRCEANITIGQSSAEVLLIVHDVPNTL	306							
QY	300	PPPTTTTTTTTTTTTTILITF-----DSRAGEGTTGAVDH	336							
Db	307	LPTTIIPSLITATVTTTVAITTSPTTSATTSIRPNALAGONGP-----DH	353							

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US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase Activity
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

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Db 2409 VYARP-PAKITWLMKACKPLQSDKFKVTSANGOKLYLFKIRETDSKYTCIATNEAGTDR 2467
 Qy 287 DMLVYVDEPTTIP-----PTTTTTTTTTTTTTTTTTTTSDRAGE 327
 Db 2468 DKVSMALVAPSEDEPNIVRITVNSGNPSTLHCAPAKGSPSPITTWLKDGNATE 2520

RESULT 2

T43290

hemiscentin precursor - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C:Accession: T43290; T20993; T24734

R:Vogel, B.E.; Hedgecock, E.M.

submitted to the EMBL Data Library, June 1998

A:Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-

A:Reference number: 222396

A:Accession: T43290

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-5198 <VOG>

A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1

R:Stulston, J.

submitted to the EMBL Data Library, December 1994

A:Accession: T20993

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-5198 <WIL>

A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A:Experimental source: clone F15G9

R:Kershaw, J.

submitted to the EMBL Data Library, December 1994

A:Reference number: 219929

A:Accession: T24734

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5198 <WIL>

A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A:Experimental source: clone T09B9

C:Genetics:

A:Gene: hlm-4; F15G9.4b

A:Map position: X

A:Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 1251/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/

Query Match 14.8%; Score 261.5; DB 2; Length 5198;

Best Local Similarity 24.6%; Pred. No. 8.3e-10;

Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;

Qy 14 VVIGGEVATISCOYKNSDSDVYQLNPKRQITFRDRLP-----KDSFQLNSSSL 69

Db 2200 VVAIKGALPFCPLD--DDK-----NEKGQITWLNKYPIDLEADARITRL---SNDR 2249

Qy 70 KSLTNVSIIDRCGRFCOLYTPQESYR-TTIVLPPNLMIDIOKD-TAVEGEEIYN 127

Db 2250 RLTILNVENDSGOYSCRKNDAGENSDFKATVLPPTIIMLDKDKNTAVEHSVTLS 2309

Qy 128 CTAMASKPATTTIRWFG-----NKELGKSEVEWSDMTVTYSOLMLKVKR 173

Db 2310 CPA-NGKPEPDTWFKDEGAHIENIADITIPGELNG-----NQLKITRIK 2354

Qy 174 EDDGVPVICOVHRPAVTGMLQTKYLEVOYKPOVH---IQMTYPLQGLTREGDAEPLTCE 230

Db 2335 ESDAGKYTCCEANSA--GSVEQDVVWNVYTIPIKIKDGPSPYEQ---QMERVVISCP 2408

Qy 231 AIGKPOPVVTVVRVDDDEMPQHAVL---SGPNLFNNLNKTDNGYRCEASNIYKKAHS 286

Db 2409 VYARP-PAKITWLMKACKPLQSDKFKVTSANGOKLYLFKIRETDSKYTCIATNEAGTDR 2467

Qy 287 DIMLVYDEPTTIP-----PTTTTTTTTTTTTTTTTTTTSDRAGE 327

Db 2468 DKVSMALVAPSEDEPNIVRITVNSGNPSTLHCAPAKGSPSPITTWLKDGNATE 2520

RESULT 3

T08732

hypothetical protein DKFZp566B0846.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C:Accession: T08732

R:Ottenwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: 216474

A:Accession: T08732

A:Molecule type: mRNA

A:Residues: 1-407 <OTW>

A:Cross-references: EMBL:AL050071

A:Experimental source: fetal kidney; clone DKFZp566B0846

C:Genetics:

A:Note: DKFZp566B0846.1

Query Match 13.9%; Score 245; DB 2; Length 407;

Best Local Similarity 27.7%; Pred. No. 5.3e-10;

Matches 77; Conservative 43; Mismatches 116; Indels 42; Gaps 10;

Qy 82 GRFCOLYTPD--POESYTTIVLPPNLMIDIOKTAVEG--EEIEVNCATAMASKPAT 137

Db 2 GKTKCAVTFPLGNQOSTTIVLVPEYSLIK-GPDSLIDGNGENVAALCAATGKPYA 60

Qy 138 TIRWFGKNEKLGKSEVEWSDMY-----TVTSQMLKVKHEDDGVVICOVHRPAVTGN 192

Db 61 HLDW-EGD-----LGEMESTTTSFPMETATIIISQYKLPTRPARGRRICVYKHPALERD 114

Qy 193 LQTKRYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEALICRQPRVTVWVYDDMPQH 252

Db 115 IIRSFILDIQYAVEVSVTYDGNMFVGRKG--VNKKCNADANPPKSVWSRLDGQWPDG 172

Qy 253 AVLSGPNL-FINNLNKTNDGTYRCEASNIYKKAHSDMYLVYVDP--TTIRP----- 301

Db 173 LASDVTILFVHPLTFNYSGVYICKYTNLSGRSDQKXYIYIDPRTTTLQPLTIQWHPST 232

Qy 302 -----PTTTTTTTTTTTTTTTTTTTSDRAGE 326

Db 233 ADIEDLATEPKKLPPLSTLATIKDPTIATIASVVG 270

RESULT 4

JEO099

neural cell adhesion molecule 1 - African clawed frog

N:Alternate names: N-CAM 1

C:Species: Xenopus laevis (African clawed frog)

C:Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: JEO099

R:Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohara, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A:Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the

A:Reference number: JEO099; MUID:98204770; PMID:9535795

A:Accession: JEO099

A:Molecule type: mRNA

A:Residues: 1-725 <KUD>

A:Cross-references: DBJ:AB008162; NID:g3116226; PIDN:BA025931.1; PID:g3116227

A:Experimental source: heart

C:Comment: This protein mediates and regulates various cell-cell interactions through

F:413-475/Domain: Immunoglobulin homology <IMH>

F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 13.5%; Score 238; DB 2; Length 725;

Best Local Similarity 26.2%; Pred. No. 3.4e-09;

Matches 89; Conservative 61; Mismatches 146; Indels 42; Gaps 15;

Qy 12 KDVTIEGEVATISC--QVN--KSDSVIQLN---PNRQITVFRDPRFLKDSRQL 61

Db 2409 VYARP-PAKITWLMKACKPLQSDKFKVTSANGOKLYLFKIRETDSKYTCIATNEAGTDR 2467

Qy 287 DIMLVYDEPTTIP-----PTTTTTTTTTTTTTTTTTTTSDRAGE 327

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:42 ; Search time 9 Seconds
(without alignments)
1548.450 Million cell updates/sec

Title: US-09-778-187b-4_COPY_21_356

Perfect score: 1765
Sequence: 1 IPTGDCGNLFRKDYVIEGE.....LTIITDSRAGEGTIGAVDH 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	13.3	1088	1 NCAL_XENLA	P16170 xenopus lae
2	226.5	12.8	515	1 PVR1_PIG	O94176 sus scrofa
3	225.5	12.6	837	1 NCAL_MOUSE	O35136 mus musculu
4	223	12.6	344	1 NTRI_RAT	O62718 rattus norv
5	222	12.6	530	1 PVR2_MOUSE	P32507 mus musculu
6	222	12.6	1092	1 NCAL_XENLA	P36305 xenopus lae
7	220	12.5	337	1 G55A_CHICK	O98892 gallus gall
8	220	12.5	417	1 PVR_CERAE	P32506 cercopithe
9	220	12.5	538	1 PVR2_HUMAN	O92892 homo sapien
10	218.5	12.4	517	1 PVR1_HUMAN	O15223 homo sapien
11	217	12.3	417	1 PVR_HUMAN	P15151 homo sapien
12	215.5	12.2	837	1 NCAL_MOUSE	O15394 mus musculu
13	211	12.0	847	1 CD22_HUMAN	P20273 homo sapien
14	211	12.0	4393	1 PGBM_HUMAN	P98160 homo sapien
15	209.5	11.9	345	1 OPRM_BOVIN	P11834 bos taurus
16	209	11.8	1242	1 NPHN_MOUSE	O94287 mus musculu
17	208.5	11.8	353	1 CEFU_CHICK	O90773 gallus gall
18	207.5	11.8	345	1 OPRM_HUMAN	O14982 homo sapien
19	207	11.7	1493	1 NEOL_MOUSE	P97798 mus musculu
20	206.5	11.7	862	1 CD22_MOUSE	P33329 mus musculu
21	204	11.6	702	1 CEAS_HUMAN	P06731 homo sapien
22	203	11.5	1461	1 NEOL_HUMAN	O92859 homo sapien
23	202	11.4	515	1 PVR1_MOUSE	O91466 mus musculu
24	202	11.4	1443	1 NEOL_CHICK	O90610 gallus gall
25	201.5	11.4	345	1 OPRM_RAT	P32736 rattus norv
26	199	11.3	338	1 LAMP_CHICK	O98919 gallus gall
27	198	11.2	1377	1 NEOL_RAT	P97603 rattus norv
28	197	11.2	583	1 C166_MOUSE	O61490 mus musculu
29	194.5	11.0	3707	1 PGBM_MOUSE	O05793 mus musculu
30	194	11.0	1091	1 NCAL_CHICK	P13590 gallus gall
31	193	10.9	761	1 NCAL_HUMAN	P13591 homo sapien
32	193	10.9	848	1 NCAL_HUMAN	P13591 homo sapien
33	192	10.9	1036	1 AKOL_CHICK	P28685 gallus gall

34	191.5	10.8	583	1 C166_HUMAN	Q13740 homo sapien
35	189.5	10.7	646	1 MO18_HUMAN	P43121 homo sapien
36	189	10.7	853	1 NCAL_BOVIN	P31836 bos taurus
37	189	10.7	588	1 NCAL_RAT	P13596 rattus norv
38	188	10.7	588	1 C166_CHICK	P42292 gallus gall
39	188	10.7	1447	1 DCC_MOUSE	P70211 mus musculu
40	187.5	10.6	338	1 LAMP_HUMAN	Q13449 homo sapien
41	185.5	10.5	338	1 LAMP_RAT	O62813 rattus norv
42	185.5	10.5	764	1 ICCR_DROME	O08180 drosophila
43	185.5	10.5	1234	1 NPHN_RAT	O91044 rattus norv
44	185.5	10.5	1241	1 NPHN_HUMAN	O60500 homo sapien
45	182.5	10.3	2012	1 DSCA_HUMAN	O60469 homo sapien

ALIGNMENTS

RESULT 1
NCAL_XENLA STANDARD: PRT: 1088 AA.
ID P16170;
AC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neutral cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180).
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90098871: PubMed-2481269;
RA Kriegl P.A., Sakaguchi D.S., Kintner C.R.;
RT "Primary structure and developmental expression of a large cytoplasmic domain form of Xenopus laevis neural cell adhesion molecule (NCAM)."
RT Nucleic Acids Res. 17:10321-10335(1989).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; N-CAM 180 (shown here) and N-CAM 140; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL TISSUE.
CC -1- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M25696; AAA49909.1; .
DR PIR: S09600; IJXNL.
DR HSP: P56276; ITIK.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003598; IG_C2.
DR Pfam: PF000441; fn3; 2.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00408; IGc2; 5.

KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1088
FT DOMAIN 20 705
FT DOMAIN 706 723
FT DOMAIN 724 1088
FT DOMAIN 134 100
FT DOMAIN 129 193
FT DOMAIN 225 289
FT DOMAIN 315 386
FT DOMAIN 413 480
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
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FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
FT VARSPLIC 804 1049
SQ SEQUENCE 1088 AA; 117778 MW; 627385B03F3E83 CRC64;

Query Match 13.3%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 5.9e-10;
Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

QY 12 KDVTVEGEVATITSC---QVNSK---DDSVYQLN---PNRQITVFDRFPLKDSRFOL 61
DB 199 KDIQVIVNPPPTIOARQLRNATANNAESVYLSCDADGFPDPDISMLKKEPIEDGE-EK 257
QY 62 LNFSSSEKLKSLTNVSIISDGRYFCOLYTPDPOESYTTITVLPRLNLMIDIKDVAVES 121
DB 258 ISNENQSEHTIHVEKDEDAEISC-IANNQGEAEHTILKAYAPKITYVENKRAVEL 316
QY 122 EEIEVNCTAMASKPATITFMFGKNKE-----LKGKSEVEEMSDYTVTSQMLRVHKE 174
DB 317 DEITLFCFA-SGDPISPISTWRAVNISSEATTLGDHIYVKEHIRM---SALTLDIQY 371
QY 175 DCGVPYICQVEHPAVNGNLOTQRYLEVQYKPOVHIQMTYPLQGLTRBGDAFELTCEAIGK 234
DB 372 TDAGEYFCIASNP-IGVDAQM-YFEVOYAPKIR---GPVVVYTWEGNPNVTICCEFAH 425
QY 235 POFVMTWYRVDEEMPOH-----AVLSGP---NLFINLNKKTNGTYRCFASNIYVKAHS 286
DB 426 PR-AAVTWFRDGLLSNSFNKIKITSGPSSSELEVNPDSEDFGNYNCTAINTIGHFS 484
QY 287 DYMLVYVDPTTIPPTTT 326
DB 485 EFLIVQADTPSS---PAIRKVEPYSTVMIVFDEPDSTG 521

RESULT 2
PVAL_PIG STANDARD; PRT: 515 AA.

AC 09GL76;
DT 16-OCT-2001 (Rel. 40. Created)
DT 16-OCT-2001 (Rel. 40. Last sequence update)
DT 15-JUN-2002 (Rel. 41. Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).
GN PVAL1 OR PRL1 OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.,
RT "Porcine HvEC, a member of the highly conserved HvEC/nectin 1 family,
is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
CC -1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CELLS.
CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC EMBL: AF08632; AAC30281.1; -.
DR HSSP: P06907; 1NEU
DR InterPro: IPR003559; Ig.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003596; Ig_Like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig_3.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00408; IgC2; 2.
DR SMART: SM00406; IgV; 1.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 31 355
FT DOMAIN 356 376
FT DOMAIN 377 515
FT DOMAIN 44 131
FT DOMAIN 165 233
FT DOMAIN 262 323
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
SQ SEQUENCE 515 AA; 57047 MW; BFA00320DDE3785 CRC64;

Query Match 12.8%; Score 226.5; DB 1; Length 515;
Best Local Similarity 25.4%; Pred. No. 8.3e-10;
Matches 79; Conservative 49; Mismatches 132; Indels 51; Gaps 12;

QY 14 VVIEGEVATISQVWKSDDSVYQLNPNRQITVFDRFPLKDSRFOLNFSSELSKVS 73
DB 62 ITQVWQKATNSKQN-----VAIYNPAMGVSVALAPY-----EREPLRSPFTGTSTIL 111
QY 74 TNVSIISDEGRYFCOLYTPDP---QESYTTITVLPRLNLMIDIQ-----KDVAVEGEE 123

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 ; Search time 28.5 Seconds
(without alignments)
2429.187 Million cell updates/sec

Title: US-09-778-187b-4_COPY_21_356

Perfect score: 1765
Sequence: 1 IPTGGGQNLFTKDVYIEGE.....LTITDSRAGEGTCIGAVDH 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	445	11	Q8R4L1
2	1749.5	99.1	456	11	Q8R5M8
3	1749.5	99.1	494	11	Q8CRV3
4	1738	98.5	442	4	Q9B167
5	1541	87.3	336	11	Q9D6E7
6	1204	68.2	295	11	Q922H8
7	1171.5	66.4	306	11	Q9QYL4
8	1151	65.2	295	11	Q9QYL6
9	1062	60.2	289	11	Q9QYL5
10	1038.5	58.8	278	11	Q9QYL3
11	624	35.4	388	11	Q8R464
12	611	34.6	381	4	Q9Y4A4
13	480.5	27.2	396	11	Q9N28
14	467.5	26.5	432	4	Q9UJPI
15	298	16.9	549	11	Q9D006
16	295	16.7	549	11	Q9JLB8

17	289	16.4	549	4	Q9NOS3	Q9NOS3 homo sapien
18	274.5	15.6	438	11	Q9JLB7	Q9JLB7 mus musculu
19	274.5	15.6	510	11	Q9JLB8	Q9JLB8 mus musculu
20	261.5	14.8	5198	5	Q76518	Q76518 caenorhabd1
21	252	14.3	439	13	Q57349	Q57349 gallus gall
22	245	13.9	407	4	Q9Y412	Q9Y412 homo sapien
23	239	13.5	1482	5	Q9V4Y0	Q9V4Y0 drosophila
24	238	13.5	725	13	Q73633	Q73633 xenopus lae
25	234	13.3	393	4	Q95727	Q95727 homo sapien
26	228.5	12.9	7962	4	Q10465	Q10465 homo sapien
27	228.5	12.9	34350	4	Q8W242	Q8W242 homo sapien
28	226	12.8	4162	13	Q98918	Q98918 gallus gall
29	222	12.6	725	13	Q73634	Q73634 xenopus lae
30	221	12.5	344	4	Q9P121	Q9P121 homo sapien
31	220	12.5	344	13	Q9DF61	Q9DF61 gallus gall
32	220	12.5	467	11	Q91VW9	Q91VW9 mus musculu
33	220	12.5	1675	13	Q98SW4	Q98SW4 brachydanto
34	219.5	12.4	1270	5	Q9J3P2	Q9J3P2 caenorhabd1
35	219	12.4	344	11	Q99PU0	Q99PU0 mus musculu
36	219	12.4	449	4	Q9UE16	Q9UE16 homo sapien
37	219	12.4	1380	4	Q9HCK4	Q9HCK4 homo sapien
38	217	12.3	417	4	Q96BJ1	Q96BJ1 homo sapien
39	216.5	12.3	605	4	Q96J84	Q96J84 homo sapien
40	216	12.2	1060	11	Q9QZ13	Q9QZ13 rattus norv
41	215	12.2	1032	13	Q8UVD6	Q8UVD6 brachydanto
42	214	12.1	413	5	Q9VAR6	Q9VAR6 drosophila
43	214	12.1	1011	5	Q24273	Q24273 drosophila
44	214	12.1	1079	5	Q9VNP2	Q9VNP2 drosophila
45	214	12.1	1102	11	Q923W7	Q923W7 mus musculu

ALIGNMENTS

RESULT 1
Q8R4L1 PRELIMINARY: PRT: 445 AA.
AC Q8R4L1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tumor suppressor in lung cancer 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of murine orthologue of the TSLC1 gene."
RL Submitted (OCF-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF343663; AAL86736.1; -; C5D5A070DAF70E55 CRC64;
SQ SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;

Query Match 100.0%; Score 1765; DB 11; Length 445;
Best Local Similarity 100.0%; Pred. No. 7.3e-139;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGGGQNLFTKDVYIEGEVATISCVYKSDSVIQLNPNRQITTFRFRPLKDSRQ 60
|||||
DB 42 IPTGGGQNLFTKDVYIEGEVATISCVYKSDSVIQLNPNRQITTFRFRPLKDSRQ 101
|||||
QY 61 LNFSSSELKVSILTNVISDEGRFCOLYTDPPQESTYTTIVLVPPRLMLIDOKTAAVE 120
|||||
DB 102 LNFSSSELKVSILTNVISDEGRFCOLYTDPPQESTYTTIVLVPPRLMLIDOKTAAVE 161
|||||
QY 121 GEEIEVNCAMASKPATTTIRWFKGNELKGSVEEDMSDWTYSQMLKVKHEDDGVPY 180
|||||
DB 162 GEEIEVNCAMASKPATTTIRWFKGNELKGSVEEDMSDWTYSQMLKVKHEDDGVPY 221
|||||
QY 181 TCGVEHPATVGNQTORVYLEVQKRPVYHQMTPPLOGLTREGAFELTCAIGKPPVWY 240
|||||

Db 222 ICVEHPAVTGNLQOTRYLEVQYKPOVHIOMTYRPLQGLTREGDAFELTCEAIKGPQVW 281
OY 241 TWRVDEMPQHAHVLGSPNLFINNLTNDNGTYRCEASNIVGAHSDYMLVYDPTTIP 300
Db 282 TWRVDEMPQHAHVLGSPNLFINNLTNDNGTYRCEASNIVGAHSDYMLVYDPTTIP 341
OY 301 PPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 336
Db 342 PPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 377

RESULT 2
085M8
ID 085M8 PRELIMINARY: PRT: 456 AA.
AC 085M8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE RA175.
GN RA175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Momoi T.;
RT "Biological function of RA175, a new member of immunoglobulin super family.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB064265; BAB3501.2; -
SQ SEQUENCE 456 AA: 49787 MW: 32268664B4BC1C7F CRC64;

Query Match 99.1%; Score 1749.5; DB 11; Length 456;
Best Local Similarity 96.8%; Pred. No. 1.5e-137;
Matches 336; Conservative 0; Mismatches 0; Indels 11; Gaps 1;

OY 1 IPTGDCQNLFTKDVYIEGVATISQVNSDSVQLNPNRQTYFRDPRFKDSRFQ 60
Db 42 IPTGDCQNLFTKDVYIEGVATISQVNSDSVQLNPNRQTYFRDPRFKDSRFQ 101
OY 61 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTIVLVPPRNLMIDIOKTAVE 120
Db 102 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTIVLVPPRNLMIDIOKTAVE 161
OY 121 GEEIEVNCPTAMASKPATTTIRMFNGKNEKLGKSEVEEMSDMTYTSQMLKVHKEDGVPV 180
Db 162 GEEIEVNCPTAMASKPATTTIRMFNGKNEKLGKSEVEEMSDMTYTSQMLKVHKEDGVPV 221
OY 181 ICVEHPAVTGNLQOTRYLEVQYKPOVHIOMTYRPLQGLTREGDAFELTCEAIKGPQVW 240
Db 222 ICVEHPAVTGNLQOTRYLEVQYKPOVHIOMTYRPLQGLTREGDAFELTCEAIKGPQVW 281
OY 241 TWRVDEMPQHAHVLGSPNLFINNLTNDNGTYRCEASNIVGAHSDYMLVYDPTTIP 300
Db 282 TWRVDEMPQHAHVLGSPNLFINNLTNDNGTYRCEASNIVGAHSDYMLVYDPTTIP 341
OY 301 PPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 336
Db 342 PPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 388

RESULT 3
09CRV3
ID 09CRV3 PRELIMINARY: PRT: 494 AA.
AC 09CRV3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 310000108RIK protein (Fragment).
GN IGSP4 OR 3100001108RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schramm L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamuya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-Oka K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,
RA Suzuki H., Toyo-Oka K., Wang K. H., Weltz C., Whitaker C., Wilmink L.,
RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK013911; BAB29050.1; -
DR MGD; MGI:1869272; Igsf4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_3.
DR SMART: SM00408; ITC2; 3.
DR SMART: SM00410; IG_Like; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 494 AA: 53946 MW: F5E09ABA1857ABCO CRC64;

Query Match 99.1%; Score 1749.5; DB 11; Length 494;
Best Local Similarity 96.8%; Pred. No. 1.7e-137;
Matches 336; Conservative 0; Mismatches 0; Indels 11; Gaps 1;

OY 1 IPTGDCQNLFTKDVYIEGVATISQVNSDSVQLNPNRQTYFRDPRFKDSRFQ 60
Db 80 IPTGDCQNLFTKDVYIEGVATISQVNSDSVQLNPNRQTYFRDPRFKDSRFQ 139
OY 61 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTIVLVPPRNLMIDIOKTAVE 120
Db 140 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTIVLVPPRNLMIDIOKTAVE 199
OY 121 GEEIEVNCPTAMASKPATTTIRMFNGKNEKLGKSEVEEMSDMTYTSQMLKVHKEDGVPV 180
Db 200 GEEIEVNCPTAMASKPATTTIRMFNGKNEKLGKSEVEEMSDMTYTSQMLKVHKEDGVPV 259
OY 181 ICVEHPAVTGNLQOTRYLEVQYKPOVHIOMTYRPLQGLTREGDAFELTCEAIKGPQVW 240
Db 260 ICVEHPAVTGNLQOTRYLEVQYKPOVHIOMTYRPLQGLTREGDAFELTCEAIKGPQVW 319
OY 241 TWRVDEMPQHAHVLGSPNLFINNLTNDNGTYRCEASNIVGAHSDYMLVYDPTTIP 300
Db 320 TWRVDEMPQHAHVLGSPNLFINNLTNDNGTYRCEASNIVGAHSDYMLVYDPTTIP 379
OY 301 PPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 336
Db 380 PPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 426

RESULT 4
09BY67
ID 09BY67 PRELIMINARY: PRT: 442 AA.
AC 09BY67;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Necilin-like protein 2.
 GN NECIL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin
 RT superfamily";
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF132811; AAF69029.1; -
 DR InterPro: IPR003599; Ig_1.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00409; IG: 3.
 DR SMART: SM00408; IGC2: 3.
 DR SMART: SM00410; IGLike: 2.
 KW Immunoglobulin domain.
 SO SEQUENCE 442 AA; 48537 MW; 68183E328735062 CRC64;

Query Match 98.5%; Score 1738; DB 4; Length 442;
 Best Local Similarity 98.5%; Pred. No. 1.3e-136;

Matches 331; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGGQNLFTKDVYIEGEVATISQVNVKSDSVYQLNPNRQTYFRDPRPLKDSRQ 60
 DB 39 IPTGGQNLFTKDVYIEGEVATISQVNVKSDSVYQLNPNRQTYFRDPRPLKDSRQ 98
 QY 61 LNFSSSEKSLVNTVSDSEGRFCQLYTPDPQESYTTITVLPVPRNLMIDIOKDTAVE 120
 DB 99 LNFSSSEKSLVNTVSDSEGRFCQLYTPDPQESYTTITVLPVPRNLMIDIOKDTAVE 158
 QY 121 GEIEVNCNTAMSKPATITRMFKGNKELKGSEVEBMSDMYVTVSOLMLKVKHEDDGVPV 180
 DB 159 GEIEVNCNTAMSKPATITRMFKGNKELKGSEVEBMSDMYVTVSOLMLKVKHEDDGVPV 218
 QY 181 ICQVEHPAVTGNLQORYLEVOYKPOVHIOMTYPLQGLTRREGDAELTCEAIGKQPQVNV 240
 DB 219 ICQVEHPAVTGNLQORYLEVOYKPOVHIOMTYPLQGLTRREGDAELTCEAIGKQPQVNV 278
 QY 241 TTVRRVDDDEMPQHAVALSGPMLFINNLKNTDNGTYRCEASNIYKKAHSDYMLVYDPTTIP 300
 DB 279 TTVRRVDDDEMPQHAVALSGPMLFINNLKNTDNGTYRCEASNIYKKAHSDYMLVYDPTTIP 338
 QY 301 PPTTT 336
 DB 339 PPTTT 374

RESULT 5

Q9D6E7 PRELIMINARY: PRT: 336 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 2900073G06RIK protein.
 GN IGSP4 OR 2900073G06RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
 RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehle T.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
 RA Schiml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
 RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guskinich S., Hill D., Holmann M., Hume D. A., Kamuya M., Lee N. H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberechts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K. P.,
 RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AK013775; BAB28988.1; -
 DR MGI: 1889272; IgSF4.
 DR InterPro: IPR003599; Ig_1.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00409; IG: 3.
 DR SMART: SM00408; IGC2: 3.
 DR SMART: SM00410; IGLike: 1.
 KW Immunoglobulin domain.
 SO SEQUENCE 336 AA; 37157 MW; FE887FA4EFD120 CRC64;

Query Match 87.3%; Score 1541; DB 11; Length 336;
 Best Local Similarity 100.0%; Pred. No. 2.3e-120;

Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPTGGQNLFTKDVYIEGEVATISQVNVKSDSVYQLNPNRQTYFRDPRPLKDSRQ 60
 DB 42 IPTGGQNLFTKDVYIEGEVATISQVNVKSDSVYQLNPNRQTYFRDPRPLKDSRQ 101
 QY 61 LNFSSSEKSLVNTVSDSEGRFCQLYTPDPQESYTTITVLPVPRNLMIDIOKDTAVE 120
 DB 102 LNFSSSEKSLVNTVSDSEGRFCQLYTPDPQESYTTITVLPVPRNLMIDIOKDTAVE 161
 QY 121 GEIEVNCNTAMSKPATITRMFKGNKELKGSEVEBMSDMYVTVSOLMLKVKHEDDGVPV 180
 DB 162 GEIEVNCNTAMSKPATITRMFKGNKELKGSEVEBMSDMYVTVSOLMLKVKHEDDGVPV 221
 QY 181 ICQVEHPAVTGNLQORYLEVOYKPOVHIOMTYPLQGLTRREGDAELTCEAIGKQPQVNV 240
 DB 222 ICQVEHPAVTGNLQORYLEVOYKPOVHIOMTYPLQGLTRREGDAELTCEAIGKQPQVNV 281
 QY 241 TTVRRVDDDEMPQHAVALSGPMLFINNLKNTDNGTYRCEASNIYKKAHSDYMLVY 293
 DB 282 TTVRRVDDDEMPQHAVALSGPMLFINNLKNTDNGTYRCEASNIYKKAHSDYMLVY 334

RESULT 6

Q922H8 PRELIMINARY: PRT: 295 AA.

DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Necilin-like protein 2.
 GN IGSP4 OR NECIL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Zhou Y, Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel cDNA encoding a member of immunosuperfamily.",
RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.
DR EMBL: AF061260; AAC6243.1; -.
DR MGD; MG1:1889272; IgSf4.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-1like.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00294; 4.Im; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_1like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 295 AA; 32309 MW; 9DE9D86F6FF6F488 CRC64;

Query Match	68.2%	Score 1204;	DB 11;	Length 295;
Best Local Similarity	100.0%;	Pred. No. 2.4e-92;		
Matches 227; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	110	MIDLOKTAVEGEIEIVNCSTAMSKPATYTRWFGNKELGKSVEEWSMITYVSOLML	169
Dd	1	MIDLOKTAVEGEIEIVNCTIMASKPATYTRWFKNKELGKSVEEWSMITYVSOLML	60
Qy	170	KVHKEDDGVPIVCVEHPAYTGNLQTORYLEVOYKPPVHAIOMTYPLDGLREGDAFLTC	229
Dd	61	KVKHEDDGVPIVCVEHPAYTGNLQTRLLEYOYKPPVHTIOMTYPLQGLRREDAFELTC	120
Qy	230	EAIKKPQPWMTWRVYDEDMPOHNVLSGPNUFLNNLNKKTNGTYRCFAASNIYKAHSIDYM	289
Dd	121	EAIKKPQPWMTWRVYDEDMPOHANVLSGPNULFNLNKKTNGTYRCFAASNIYKAHSIDYM	180
Qy	290	LXVVDPTTIPTTTTTTTTTTTTTTTTTLIITTSRAAGEECTICAVDH	336
Dd	181	LYVVDPTTIPTTTTTTTTTTTTTTTTTLLIITTSRAAGEECTICAVDH	227

RESULT 7	
Q9QYL4	
ID Q9QYL4	PRELIMINARY;
	PRT; 306 AA

DT DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DN Adhesion protein RAI175C.
GN IGSf4 OR RAI175C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
RT Momoi T.;
RL "RAI15, a novel neuron specific adhesion protein.",
EMBL: AB021966; BAA87916.1; -.
DR MGD; MGI:1889272; Igsf4.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003585; Neurexin-like.
PR Pfam: PF00047; Ig_2.
DR SMART; SM00294; 4.Im; 1.
DR SMART; SM00408; IGS2; 1.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;

Query Match	66.4%;	Score 1171.5;	DB 11;	Length 306;
Best Local Similarity	-94.1%;	Pred. No. 1.3e-89;		
Matches 224; Conservative	1;	Mismatches 2;	Indels 11;	Gaps 1;

[illegible]

RESULT 8	
Q9QYL6	
ID Q9QYL6	PRELIMINARY;
Q9QYL6	PRT; 295 AA

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RAI175a.
GN IGSF4 OR RAI175a.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kuroku Y., Momoi M.,
RA Momoi T.;
RL RAI175, a novel neuron specific adhesion protein.":
EMBL: AB021964; BAA07914.1; -;
DR MGD; MG1:1889272; IGSf4.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_LMC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam: PF00047; Ig_2.
DR SMART; SM00294; 4.Im1.1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 295 AA; 32347 MW; FDD9EB8145C6B971B CRC64;

Query Match	65.28;	Score 1151;	DB 11;	Length 295;
Best Local Similarity	95.68;	Pred. No. 6.2e-88;		
Matches 217;	Conservative	2;	Mismatches 8;	Indels 0;
			Gaps	0;

QY	110	MIDJQKTAAGEEIEYNCTAMAKPATTIRMEFGNKELGKSEVEBMSOMTYVSQML	169
Db	1	MIDJQKTAAGEEIEYNCTAMAKPATTIRMEFGNKELGKSEVEBMSOMTYVSQML	60
QY	170	KVHKEDDGVPICQVEHPAATGNLQTORYLEVQYKPOVHIOMTYPILOGLTREGDAEELTC	229
Db	61	KVHKEDDGVPICQVEHPAATGNLQTORYLEVQYKPOVHIOMTYPILOGLTREGDAEELTC	120
QY	230	EATKCPQPVAVTWVRVDEDEMPQHAVALSGPMLFINNLKNTDNGTYRCEASNTYKASHSDYA	289
Db	121	EATKCPQPVAVTWVRVDEDEMPQHAVALSGPMLFINNLKNTDNGTYRCEASNTYKASHSDYA	180
QY	290	LYVVDPEPTTIPRPTTTTTTTTTTTTTLTIITDSRAGEECTIAVAOH	336
Db	181	LYVVDPEPTTIPRPTTTTTTTTTTTTTLTIITDSRAGEECTIAVAOH	227

RESULT 9
Q9QYL5 PRELIMINARY; PRT; 289 AA
ID Q9QYL5

AC 090YL5; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adhesion protein RAI175b.
GN IGSF4 OR RAI175B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
RA Momoi T.;
RT "RA175, a novel neuron specific adhesion protein.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB021965; BAAB7915.1; -.
DR MGD; MGI:1889272; Igsf4.
DR InterPro: IPR003598; Iq_C2.
DR InterPro: IPR003600; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003585; Neurexin-Like.
DR Pfam; PF00047; Iq_2.
DR SMART; SMO0294; 4.Im; 1.
DR SMART; SMO0408; IGC2; 1.
DR SMART; SMO0410; IGC_Like; 1.
DR Immunoglobulin domain.
SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AE4A CRC64;

Query Match	60.2%	Score 1062	DB 11	Length 289
Best Local Similarity	90.3%	Pred. No. 1,6e-80		
Matches 205	Conservative	2	Missed 14	Indels 6
				Gaps 1
Qy	110	MIDIDKPTAVEEEIEVNCTAMASKRPTATIRPFKGNKELKSGSEVEWSDMYTTSQML	169	
Db	1	MIDIDKPTAVEEEIEVNCTAMASKRPTATIRPFKGNKELKSGSEVEWSDMYTTSQML	60	
Qy	170	KVHKEDDGVPLVCQENHPAVTGNLQTRKLEVOYKQVNIOMTYPLQGLTRGDAELTC	229	
Db	61	KVHKEDDGVPLVCQENHPAVTGNLQTRKLEVOYKQVNIOMTYPLQGLTRGDAELTC	120	
Qy	230	EAIGKPPQPMVTVWVWDEDEPQHAVLSCGNPLFINLNKTDNGTYRCEASINVGKASHDY	289	
Db	121	EAIGKPPQPMVTVWVWDEDEPQHAVLSCGNPLFINLNKTDNGTYRCEASINVGKASHDY	180	
Qy	290	LVVDPPTTIPPTTTTTTTTTTTTTLIIINDSRAGEGCTIGAVDH	336	
Db	181	LVVDPPTTIT-----LTIITDTTATTEPAVHDHSRAGEGCTIGAVDH	221	
RESULT	10			
Q090YL3				
ID	Q090YL3	PRELIMINARY:	PRT:	278 AA.
AC	Q090YL3			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Adhesion protein RAI175N.			
GN	IGSP4 OR RAI175N.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
OX	11			
RN	SEQUENCE FROM N.A.			
RA	Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,			
RA	Momoi T.;			
RT	"RA175", a novel neuron specific adhesion protein.";			
RL	Submitted (DEC-1998) to the EMBL/Genbank/DBD databases.			
DR	EMBL; AB021967; BAA87917.1; -			
DR	MGD; MGI:1889272; Igsf4.			
DR	InterPro; IPR003598; I9-C2.			
DR	InterPro; IPR003600; I9-1like.			

DR InterPro; IPR003306; Ig_MHC.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00294; 4.Im.1.
DR SMART; SM00408; IGC2.1.
DR SMART; SM00410; IG_1like.1.
DR Immunoglobulin domain.
KW SEQUENCE 278 AA; 30636 MW; A295FADEN2724B04 CRC64;

Query Match	58.8%	Score 1038.5	DB 11	Length 278
Best Local Similarity	88.1%	Pred. No. 1.3e-78		
Matches 200	Conservative 2	Mismatches 8	Indels 17	Gaps 1
QY 110	MIDIDKDTAVEEELIEVNCTAMASKPATPIIRFKCNKELGKSEVEEWDMDVTYSQML	169		
Db 1	MIDIDKDTAVEEELIEVNCTAMASKPATPIIRFKCNKELGKSEVEEWDMDVTYSQML	60		
QY 170	KVNKKEDDGVPLTCQVHNRAVNTGNLQTRLEVOYKRVNIOMTYPLQGLTRGDAFELTC	229		
Db 61	KVNKKEDDGVPLTCQVHNRAVNTGNLQTRLEVOYKRVNIOMTYPLQGLTRGDAFELTC	120		
QY 230	EAIGKRPQPMVTVWVNDDEMPQHAVLSCGNLPIINNLTKNKDNCTYRCEASNIYGAHSDY	289		
Db 121	EAIGKRPQPMVTVWVNDDEMPQHAVLSCGNLPIINNLTKNKDNCTYRCEASNIYGAHSDY	180		
QY 230	LYVDRPTTIPPTTTTTTTTTTTTTLTITDSRAGEGCTIGANDH	336		
Db 181	LYVDRPTTIPPTTTTTTTTTTTTTLTITDSRAGEGCTIGANDH	210		

RESULT	11			
ID	08R464	PRELIMINARY:	PRT:	388 AA.
AC	08R464;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Membrane glycoprotein.			
GN	TSLL2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniolata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ;			
RA	Fukami T., Maruyama T., Murakami Y.;			
RL	"Identification of a murine ortholog of the TSLL1-like gene 2.";			
RL	Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.			
EMBL	AY059394; AAL29692.1;			
SQ	SEQUENCE 388 AA; 42723 MW; 8E3A9DF1C3B9D23E CRC64;			

[illegible]

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Db 258 WNRGNESLPERAEVGETTLTLPGLVSADNCTYTCSEANKHGHARALVLYVDPGAVEA 317
OY 302 PTT 304
Db 318 QTS 320

RESULT 12
OY4A4 PRELIMINARY; PRT; 381 AA.
ID OY4A4:
AC OY4A4:
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE F22162_1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 2.5 Mb region in 19q13.2 containing a
RT clustered CEA/PSG gene family.";
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005525; AAC32740.1; -.
DR HSSP; P80748; 2LOI.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neutxin-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00410; Ig_Like; 2.
KW Immunoglobulin domain.
FT
FT NON_TER 1
SQ SEQUENCE 381 AA; 4187 MW; 315420B36FEDC05 CRC64;

Query Match 34.6%; Score 611; DB 4; Length 381;
Best Local Similarity 39.1%; Pred. No. 8.6e-43;
Matches 126; Conservative 62; Mismatches 120; Indels 14; Gaps 5;

OY 6 GONLFTKDVTVIEGEVATISQVNSKSDSVIQLNPNROTIFYRDFRPLKDSRFQLNFS 65
Db 2 GQGVQENVTVAAGVAELTCRLHGYDGLVYQNPARTLFEFNGRALKDERFQLEFS 61
OY 66 SSELKAVSLTNVSI SDGGRFCOLYTPPOESYTTITVLVPPRNLMIDIOKDAVEGEIE 125
Db 62 PRVRIRISDARLEDEGGYFCOLYTEDTHQJATLTLVLAPENPVEV-REQAVEGEVE 120
OY 126 VNCTAMASKPATITIMFKGKELKGKSEVEEMSDMTVTSOLMLKHKEDDGPVVCOWE 185
Db 121 LSLGLVRSRPAATLRNTRDKRELKGVSSQENGKWSVASTYFRVDRKDDGGIITICEAO 180
OY 186 HPAVGTG--NLQTORYLEVQKPOVHIOMTYRPLQGLTREGDAFELTCEATGKPOPVWTVW 243
Db 181 NQALPSGHSKQTOYLDVQYSPARIHAS---QAVYREGDTLVLTCAVNGNPPRNDIRNN 237
OY 244 RVDDEMPQAHVLSGNLFINLNKTNDNGTYRCEASNIYKASHSDVWLYYDP---PTT- 298
Db 238 RGNESLPERAEVGETTLTLPGLVSADNCTYTCSEANKHGHARALVLYVYGGESRLPTEG 297
OY 299 ---IPPTTTTTTTTTTTTTTIL 317
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Db 298 GGCAPPDGAIVEAQTSVPYAIIV 319
RESULT 13
OY9N28 PRELIMINARY; PRT; 396 AA.
ID OY9N28:
AC OY9N28:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein).
GN NECT1 OR TSIL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RT "Cloning and expression analysis of novel mouse cDNA encoding a
RT membrane protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of a murine ortholog of the TSIL1-like gene 1.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF195662; ANG35584.1; -.
DR EMBL; AY059393; AAL29691.1; -.
DR MGI; MGI:2137858; Nect1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IgC2; 3.
DR SMART; SM00410; Ig_Like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 396 AA; 42964 MW; C1ADF8B57D141F3A CRC64;

Query Match 27.2%; Score 480.5; DB 11; Length 396;
Best Local Similarity 35.0%; Pred. No. 6.8e-32;
Matches 109; Conservative 64; Mismatches 119; Indels 19; Gaps 7;

OY 5 DGONLFTKDVTVIEGEVATISQVNSKSDSVIQLNPNROTIFYRDFRPLKDSRFQLNFS 64
Db 27 DDSQPTSDETVYAGGTVYVKCVKDHDSISQWNSNPAQOTLTFGKRALDRKRIOLVSS 86
OY 65 SSELKAVSLTNVSI SDGGRFCOLYTPPOESYTTITVLVPPRNLMIDIOKDAVEGEIE 124
Db 87 TPHELISISNVALADEGETSIFLMPYRTAKSLVTYVIGIQKPLITYSKSLRKEKTA 146
OY 125 EVNCTAMASKPATITIMFKGKELKGKSEVEEMSD--MYTYSQMLVKHKEDDGVPI 181
Db 147 TLNCSGSGSKPAQALTWKRGDDELHGDQTRIEDPNGKTFEYSSVSFQVTRDEDDANIV 206
OY 182 COVEHPAVTG--NLQTORYLEVQKPOVHIOMTYRPLQGLTREGDAFELTCEATGKPOPVW 240
Db 207 CSVNHESLGGADKRSQRIEVLTYPTAMR---PEPAHNRREGOKLLHREGGNPPPOQY 263
OY 241 TWVRVDDEMP---QHAVLSGNLFINLNKTNDNGTYRCEASNIYKASHSDVWLYYDPP 296
Db 264 VVWKESSEPRPKMTQESALIFP-----FLNKDSGTGCTATSNMGSYATAYLTLLVNDPS 318
OY 297 TTIPPTTTT 307
Db 319 ---PVSSSSST 326

RESULT 14
OY9JCP1
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ID 09UPL PRELIMINARY: PRT: 432 AA.
AC 09UPL;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BK134P22.1 (Novel protein similar to mouse IMMUNOSUPERFAMILY protein
BL2) (NECTIN-like protein 1).
GN BK134P22.1 OR NECL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RP Baguley C.;
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Yuan J., Qiang B.;
RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL035403; CAB56227.1; -
DR EMBL: AF062733; AAD17540.2; -
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00294; 4.Im; 1.
DR SMART: SM00408; IGC2. 1.
DR SMART: SM00410; IG_Like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 432 AA; 47020 MW; AC474EPEC4C518C CRC64;

Query Match 26.5%; Score 467.5; DB 4; Length 432;
Best Local Similarity 34.4%; Pred. No. 9, 2e-31;
Matches 104; Conservative 65; Mismatches 122; Indels 11; Gaps 6;

QY 10 FTKDVTVEGEVATISGVNKSDDSVYQLNPNRQTIYFRDPRPKDSRFQLLNFSSSEL 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 WTSDETVVAGGVTLKQVYHDESSLSQNSNPAQOTLYFGKRALNDNRQLQVTSPIHEL 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 KSLTVNVSIDEGRYFCOLYTDPPQESYTTITVLPVRNLMIDIQDTAVEGEIEVNCI 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 SISISNVALADEEYTCSTFTMPRTAKSLVYLGIPOKRIITGYKSSLSKEKPTATLNCQ 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 AMASKPATITRMFKGNKELKSK-SEVEEMSD--MYTTSQMLKVKHKEDDGVVICOVEH 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 SSGSKPAARLTMRKKGQDELHGEPTRIQEDPNKGTFTVSSVTFQVTRDDGASIVCSVNH 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 PAVTG-NLQTORYLEVQYKRVNHIQMTYPLQGLTREGDAFELTCEAIGKPPVMTWVRV 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 ESLKGDASTSORIEVLYPTAMIRDP--HPRGQKLLHCEGRGNVPPQYLMEK- 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 DDEMPHNVLSGNLFNNLNKTDNGTYRCASNIYGAHSDMLVYDPPPTTPTT 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 304 EGSVPLKMTQESALTFPLNKSQGTGCTATSNMGSKAYVTLNVNDPS--PVSSS 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 TT 307
   : :
DB 361 ST 362

RESULT 15
09D006 PRELIMINARY: PRT: 549 AA.
AC 09D006;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 2610301B19RLK proteln.
GN 2610301B19RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamenaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann M., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuk S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK011949; BAB27933.1; -
DR MGD: MGI:1914402; 2610301B19RLK.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; IG; 1.
DR SMART: SM00410; IG_Like; 1.
SQ SEQUENCE 549 AA; 60703 MW; 327750BEC7319B32 CRC64;

Query Match 16.9%; Score 298; DB 11; Length 549;
Best Local Similarity 25.9%; Pred. No. 1, 7e-16;
Matches 93; Conservative 65; Mismatches 159; Indels 42; Gaps 11;

QY 6 GQNLFTKDVTEGEVATISC--QVKNSSDSYV--QLNPNRQTI-----YFRDPRPK 55
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 58 GSITVEPHVTAWGKNVSLKCLEVNETTQISWEIHGKSTQTVAVNHPQIGFSVQGVY 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 56 DSRFQLLNFSSSELKSLTVNVSIDEGRYFCOLYTDPP--POESYTTITVLPVRNLMIDI 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 QGVRLFNKNLSNDATITLINIGFSDSGKITCAKVTLPRLNAGSSTTVYLVVEFTVSLIK- 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 QKDTAVEG--EEIEVNCIAMASKPATITRMFKGNKELKSKSEVEEMSDMYTTSQMLKV 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 177 GPDSIDGNETVAACVCSSTGKPVADW--EGDLGEREFSTISPLNATIVSQVELPP 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 HKEDDGVVICOVEHNPVAVNGNLOTQRYLEVQYKRVNHIQMTYPLQGLTREGDAFELTCEA 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 YPRARARRITCVVKKHRALEEDIRSFILDIQYAVEVSIVGYDGNMVRGKG--VNLKCA 293
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 IGRPPVMTWVRVVDDEMPHNVLSGNPL--FINLNKTDNGTYRCASNIYGAHSDYML 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 294 DANRPFKSVMSRLDQWMDGLASDNTLHFVHRLVNVSGVYKVSNSLGRSROKXVI 353
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 YVYDPP--TTTTP-----PTTTTPTTTTPTTTTTLTTTTSRAG 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 354 YISDPPPTTTTLQPTVQMHSSPADVQDIDATENKKLPRPLSLATLTKDDTIGTIIASVVG 412
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: November 20, 2002, 07:39:02
Job time : 29.5 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 07:34:43 : Search time 62.5 Seconds
(without alignments)
716.355 Million cell updates/sec

Title: us-09-778-187b-4_copy_21_356

Perfect score: 1765
Sequence: 1 IPFGDGNLFKDYVIEGE.....LTITDSRAGECTIGAVDH 336

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	423	21	AAV45093
2	1741	98.6	402	21	AAV23691
3	1741	98.6	440	20	AAV17830
4	1741	98.6	440	21	AAV01321
5	1741	98.6	440	22	AAU29040
6	1741	98.6	442	21	AAV25619
7	1741	98.6	442	21	AAV94341
8	1741	98.6	442	21	AAV45092
9	1741	98.6	442	23	AAE19887
10	1694	96.0	364	21	AAV25586

11	1592.5	90.2	443	22	AAB88427
12	1571	89.0	414	21	AAV35028
13	1124.5	63.7	229	21	AAV25593
14	631	35.8	387	22	AAV78418
15	625.5	35.4	444	20	AAV3741
16	625.5	35.4	444	22	AAV47251
17	606	34.3	388	22	ABV11897
18	599	33.9	388	22	AAV79402
19	580.5	32.9	404	23	ABG66677
20	578.5	32.8	404	22	AAV61142
21	480.5	27.2	398	21	AAV69287
22	480.5	27.2	404	22	AAE00868
23	469.5	26.6	368	21	AAV94405
24	469.5	26.6	398	19	AAV80405
25	469.5	26.6	398	20	AAV29592
26	469.5	26.6	398	20	AAV13358
27	469.5	26.6	398	21	AAV94403
28	469.5	26.6	398	21	AAV69288
29	469.5	26.6	398	21	AAV50298
30	469.5	26.6	398	21	AAV15095
31	469.5	26.6	398	22	AAU12345
32	469.5	26.6	398	22	AAB80226
33	469.5	26.6	398	23	AAB53083
34	469.5	26.6	398	23	ABP61823
35	469.5	26.6	398	23	ABV95444
36	469.5	26.6	398	23	ABV84838
37	469.5	26.6	564	21	AAE00867
38	469.5	26.5	344	22	AAV94406
39	467.5	26.5	367	22	ABV51281
40	467.5	26.5	432	21	AAV94402
41	467.5	26.5	432	21	AAV65286
42	467.5	26.5	432	21	AAV45094
43	467.5	26.5	432	22	ABV54013
44	467.5	26.5	598	21	AAV94404
45	457	25.9	433	21	AAV53272

ALIGNMENTS

RESULT 1	
ID	AAV45093 standard; Protein; 423 AA.
AC	AAV45093;
XX	
XX	
XX	31-MAY-2000 (first entry)
DE	Mouse lymphoid derived dendritic cell adhesion molecule.
XX	
XX	Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1;
KW	B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
KW	biological activity: quality control reagent; treatment; inflammation;
KW	immune system disorder; autoimmune; viral infection; infectious disease;
KW	organ transplant rejection; bone marrow; modulator; immune response.
OS	Mus sp.
XX	
XX	
FH	
FT	Key
FT	Domain
FT	Modified-site
FT	/note= "N-Glycosylation site"
FT	83..85
FT	Modified-site
FT	/note= "N-Glycosylation site"
FT	95..97
FT	Modified-site
FT	/note= "N-Glycosylation site"
FT	147..149
FT	Modified-site
FT	/note= "N-Glycosylation site"
FT	286..288
FT	Modified-site
FT	/note= "N-Glycosylation site"
FT	290..292
FT	Modified-site
FT	/note= "N-Glycosylation site"

Human membrane or
Human secreted pro
Protein encoded by
Human protein SEQ
Beta-secretase. H
Beta-secretase. H
Human F22162_1 hom
Human protein SEQ
Human novel polype
Human NOV12 protei
Amino acid sequenc
Mouse brain immuno
Human ACAM4/IgC1-F
A secreted protein
Human MAGPI protei
Amino acid sequenc
Human ACAM cellula
Amino acid sequenc
Human LDCAM bindin
Human PRO258 polyp
Human angiogenesis
Human polypeptide
Human angiogenesis
Human PRO258 prote
Human brain immuno
Human ACAM4/IgC4-F
Human secreted pro
Human ACAM cellula
Amino acid sequenc
Human LDCAM bindin
Human secreted pro
Human ACAM6/IgC4-F
Human Beut-like 1

```
FT Domain 357..377
FT /Label= Transmembrane_domain
FT 378..423
FT /Label= Cytoplasmic_domain
XX
XX MO200008158-A2.
XX
XX 17-FEB-2000.
XX
XX 05-AUG-1999; 99WO-US17905.
XX
XX 07-AUG-1998; 98US-0095672.
XX
XX (IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC;
XX
XX WPI: 2000-205712/18.
XX N-PSDB: AA50883.
XX
XX Novel molecules designated LDCAM are capable of altering or modulating
XX T cell function -
XX
XX Claim 7; Page 46-47; 44pp; English.
XX
XX The present amino acid sequence is the mouse lymphoid derived dendritic
XX cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
XX cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
XX region of B7-1. Mouse LDCAM is found on whole embryo, testes, triple
XX negative cells murine splenic and lymph node CD8+, S49.1 and dendritic
XX cells. LDCAM polypeptides interacts with T cell surface molecules
XX to alter signalling and inhibits T cell proliferation, bind to
XX themselves and B7-1, an LDCAM binding protein and increases natural
XX killer (NK) cell populations. It may be used to measure the biological
XX activity and as quality control reagents of LDCAM binding proteins.
XX LDCAM may be used for treating disorders associated with malfunctioning
XX of immune system, inflammation, autoimmune disorders, viral infected
XX cells, infectious diseases and for killing tumour cells. They are also
XX useful for prevention or reducing the effect of organ and bone marrow
XX transplant rejection and for modulating T cell immune responses. LDCAM
XX polypeptides may also be used as carriers for delivering agents attached
XX to T cells or cells bearing B7-1.
XX
XX Sequence 423 AA:
XX
XX Query Match 100.0%; Score 1765; DB 21; Length 423;
XX Best Local Similarity 100.0%; Pred. No. 8.2e-124;
XX Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 IPFGDQNLFTKDVYIEGEVATISQVKNKSDSVIQLNPNRQTIYFDFRPLKDSRFQ 60
XX |||||||
XX 21 IPFGDQNLFTKDVYIEGEVATISQVKNKSDSVIQLNPNRQTIYFDFRPLKDSRFQ 80
XX
XX 61 LNFSSSELKSVLTNVSISDEGRFCQLTDPPOESYTTITVLVPPRNLMIDIOKDTAVE 120
XX |||||||
XX 81 LNFSSSELKSVLTNVSISDEGRFCQLTDPPOESYTTITVLVPPRNLMIDIOKDTAVE 140
XX
XX 121 GEEIEVNCATAMASKPATITRMFKGNKELKGKSEVEESDMYTVTSQMLMKVHKEDGVPV 180
XX |||||||
XX 141 GEEIEVNCATAMASKPATITRMFKGNKELKGKSEVEESDMYTVTSQMLMKVHKEDGVPV 200
XX
XX 181 ICQVEHPATGNLQTORYLEVOYKPKOVHIOMTYPILOGLTRREGDAFELTCEAIGKPPVAV 240
XX |||||||
XX 201 ICQVEHPATGNLQTORYLEVOYKPKOVHIOMTYPILOGLTRREGDAFELTCEAIGKPPVAV 260
XX
XX 241 TTVRRVDDMPQAHVYISGPNLFINNLKNTDNGTYRCASINIVGKASDYMLYYDPPTTIP 300
XX |||||||
XX 261 TTVRRVDDMPQAHVYISGPNLFINNLKNTDNGTYRCASINIVGKASDYMLYYDPPTTIP 320
XX
XX PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 336
XX |||||||
XX 321 PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 356
XX
```

```
RESULT 2
AAM23691
ID AAM23691 standard; Protein; 402 AA.
XX
XX AAM23691;
XX
XX 12-OCT-2001 (first entry)
XX
XX Human EST encoded protein SEQ ID NO: 1216.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder;
XX biodiversity; gene therapy; nutrition.
XX
XX Homo sapiens.
XX
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI: 2001-476164/51.
XX N-PSDB: AAH98350.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 20; Page 877-878; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention.
XX
XX Sequence 402 AA:
XX
XX Query Match 98.6%; Score 1741; DB 22; Length 402;
XX Best Local Similarity 98.8%; Pred. No. 4.8e-122;
XX Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 IPFGDQNLFTKDVYIEGEVATISQVKNKSDSVIQLNPNRQTIYFDFRPLKDSRFQ 60
XX |||||||
XX 39 IPFGDQNLFTKDVYIEGEVATISQVKNKSDSVIQLNPNRQTIYFDFRPLKDSRFQ 98
XX
XX 61 LNFSSSELKSVLTNVSISDEGRFCQLTDPPOESYTTITVLVPPRNLMIDIOKDTAVE 120
XX |||||||
XX 99 LNFSSSELKSVLTNVSISDEGRFCQLTDPPOESYTTITVLVPPRNLMIDIOKDTAVE 158
XX
XX 121 GEEIEVNCATAMASKPATITRMFKGNKELKGKSEVEESDMYTVTSQMLMKVHKEDGVPV 180
XX |||||||
XX 159 GEEIEVNCATAMASKPATITRMFKGNKELKGKSEVEESDMYTVTSQMLMKVHKEDGVPV 218
XX
XX 181 ICQVEHPATGNLQTORYLEVOYKPKOVHIOMTYPILOGLTRREGDAFELTCEAIGKPPVAV 240
XX |||||||
XX 219 ICQVEHPATGNLQTORYLEVOYKPKOVHIOMTYPILOGLTRREGDAFELTCEAIGKPPVAV 278
XX
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FT Modified-site 402..408 /note="N-myristoylation site"
FT Modified-site 411..417 /note="N-myristoylation site"
FT Modified-site 427..433 /note="N-myristoylation site"
FT Modified-site 428..432 /note="N-myristoylation site"
FT Modified-site 430..434 /note="N-myristoylation site"
FT Modified-site 430..434 /note="N-glycosylation site"
XX
XX
PN WO200032776-A2.
XX
PD 08-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US28301.
XX
PR 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 22-DEC-1998; 98US-0113296.
XX
XX (GENTECH) GENENTECH INC.
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
PI Hillan KJ, Kijavyn IJ, Napier MA, Roy MA, Tumas D, Wood WI;
DR WPI: 2000-412324/35.
XX N-PSDB: AAA49563.
XX
PT New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
XX
PS Claim 12; Fig 24; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources.
XX
SQ Sequence 440 AA:

Query Match 98.6%; Score 1741; DB 21; Length 440;
Best Local Similarity 98.8%; Pred. No. 5,4e-122;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDSQNLFTKDVYIEGEVATISQVKKSDSVIQLNPNQOTTYFRDPRFKDSRPQ 60
DB 37 IPTGDSQNLFTKDVYIEGEVATISQVKKSDSVIQLNPNQOTTYFRDPRFKDSRPQ 96
QY 61 LNFSSSELKVSILNVSISDEGRYFCQLYTPDPQESYTTITVLPVRNIMIDIQDPAYE 120
DB 97 LNFSSSELKVSILNVSISDEGRYFCQLYTPDPQESYTTITVLPVRNIMIDIQDPAYE 156
QY 121 GEIEVNCYAMASKPATTTIRWFKGNKEKSGSVESWMSMTYVTSOLMLKVKHEDGVPY 180
DB 157 GEIEVNCYAMASKPATTTIRWFKGNKEKSGSVESWMSMTYVTSOLMLKVKHEDGVPY 216
QY 181 ICQVEHPATGNLQDQRYLEVQYKPOVHTQMTYPLQGLRREGDAFELTCEATGKPOPVAV 240
DB 217 ICQVEHPATGNLQDQRYLEVQYKPOVHTQMTYPLQGLRREGDAFELTCEATGKPOPVAV 276
QY 241 TWRVVDDEMPQAVILSGPMLFINLNKKTNGTYRCEASNTVGKASHDYMLYVDPPTTP 300
DB 277 TWRVVDDEMPQAVILSGPMLFINLNKKTNGTYRCEASNTVGKASHDYMLYVDPPTTP 336
QY 301 PPTT 336
DR

DB 337 PPTT 372
RESULT 5
AAU29040
ID AAU29040 standard; Protein; 440 AA.
XX
XX AAU29040;
AC
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #17.
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US06520.
PF
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US15491.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GENTECH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2001-602746/68.
DR N-PSDB: AAS45941.

QY 301 PPTTTTTTTTTTTTTTTTDSRAGEGTCIGAVDH 336
 DB 339 PPTTTTTTTTTTTTTTTTDSRAGEGTCIGAVDH 374

RESULT 7
 ID AAY94341 standard; Protein; 442 AA.
 XX AAY94341;
 AC AAY94341;
 XX 22-AUG-2000 (first entry)
 DE Human cell surface receptor protein #8.
 XX
 KW Human; HCSRPs; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
 KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
 KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia;
 KW melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia;
 KW Alzheimer's diseases; multiple sclerosis; epilepsy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1..44 Location/Qualifiers
 FT /label= Signal_peptide
 FT 45..442
 FT /label= HCSR-8
 FT 57..126
 FT /label= Immunoglobulin_domain
 FT 159..222
 FT /label= Immunoglobulin_domain
 FT 260..315
 FT /label= Immunoglobulin_domain
 FT 375..394
 FT /label= Transmembrane_domain
 FT 53
 FT /note= "potential phosphorylation site"
 FT 67
 FT /note= "potential glycosylation site"
 FT 101
 FT /note= "potential glycosylation site"
 FT 103
 FT /note= "potential phosphorylation site"
 FT 113
 FT /note= "potential glycosylation site"
 FT 115
 FT /note= "potential phosphorylation site"
 FT 155
 FT /note= "potential phosphorylation site"
 FT 165
 FT /note= "potential glycosylation site"
 FT 176
 FT /note= "potential phosphorylation site"
 FT 190
 FT /note= "potential phosphorylation site"
 FT 233
 FT /note= "potential phosphorylation site"
 FT 241
 FT /note= "potential phosphorylation site"
 FT 304
 FT /note= "potential glycosylation site"
 FT 308
 FT /note= "potential glycosylation site"
 FT 310
 FT /note= "potential phosphorylation site"
 FT 329
 FT /note= "potential phosphorylation site"
 FT 368
 FT /note= "potential phosphorylation site"
 FT 432
 FT /note= "potential glycosylation site"
 XX

PN W0200028032-A2.
 XX 18-MAY-2000.
 PD 12-NOV-1999; 99WO-US26742.
 XX
 PF 12-NOV-1998; 98US-0191280.
 PR 07-DEC-1998; 98US-0206647.
 PR 08-MAR-1999; 99US-0123404.
 XX
 PA (INCYTE) INCYTE PHARM INC.
 XX
 XX Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
 PI Hillman JL, Bandman O, Azimzal Y, Au-Young J;
 PI
 DR WPI: 2000-376546/32.
 DR N-PsDB; AAA27051.
 XX
 PT New human cell surface receptor protein and polynucleotide useful for
 PT diagnosis, prevention and treatment of cancer, immune disorders,
 PT infection and neuronal disorders
 XX
 PS Claim 1; Page 81-82; 97pp; English.
 XX
 CC The present sequence is a novel human cell surface receptor protein
 CC (HCSR) designated HCSR-8. The nucleotide sequence was identified in
 CC Incyte Clone 312256 from the cDNA library LUNGNOT02, which was made from
 CC RNA isolated from lung tissue. A number of Incyte clones were used to
 CC assemble the consensus sequence. BLAST analysis showed that the sequence
 CC is homologous to immunoglobulin protein B12 93779242. HCSR and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathesia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HSCRs may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing
 CC HCSR and for diagnosis of HCSR-related disorders. HCSR and its
 CC catalytic or immunogenic fragments are useful for drug screening using
 CC libraries of compounds.
 CC
 SQ Sequence 442 AA:
 Query Match 98.6%; Score 1741; DB 21; Length 442;
 Best Local Similarity 98.8%; Pred. No. 5.4e-122;
 Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDCQNLFTKDVTVIEGEVATISCOVKNKSDSVIQLNPNRQITFRDFPLKDSRPQ 60
 DB 39 IPTGDCQNLFTKDVTVIEGEVATISCOVKNKSDSVIQLNPNRQITFRDFPLKDSRPQ 98

QY 61 LNFSSSELKVSITNVSISDEGRYFCQLYTDPPQESYTTITVLPVPRNLMIDIOKDAVE 120
 DB 99 LNFSSSELKVSITNVSISDEGRYFCQLYTDPPQESYTTITVLPVPRNLMIDIOKDAVE 158

QY 121 GEEIEVNCCTAMASKPATTTTRWFKGNKELKGSVEEWSMYYVTSQLMKVKKEDGQVY 180
 DB 159 GEEIEVNCCTAMASKPATTTTRWFKGNKELKGSVEEWSMYYVTSQLMKVKKEDGQVY 218

QY 181 ICQVEHPATGNLQDQRYLEVQKPPQVHITQMTYPLQGLTREGDAELTCEAIGKPPQVAY 240
 DB 219 ICQVEHPATGNLQDQRYLEVQKPPQVHITQMTYPLQGLTREGDAELTCEAIGKPPQVAY 278

QY 241 TWVRVDEKPPQAVLISGPNLFTNNLKTNDNGTYRCEASNIIVKAKSDYMLVYDPTTIP 300
 DB 279 TWVRVDEKPPQAVLISGPNLFTNNLKTNDNGTYRCEASNIIVKAKSDYMLVYDPTTIP 338

QY 301 PPTTTTTTTTTTTTTTTTDSRAGEGTCIGAVDH 336
 DB 339 PPTTTTTTTTTTTTTTTTDSRAGEGTCIGAVDH 374

XX	RESULT 8
XX	AAV45092
XX	AAV45092 standard; Protein; 442 AA.
AC	AAV45092;
XX	
DT	31-MAY-2000 (first entry)
XX	
DE	Human lymphoid derived dendritic cell adhesion molecule.
XX	
KW	Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
KW	B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
KW	biological activity; quality control reagent; treatment; inflammation;
KW	immune system disorder; autoimmune; viral infection; infectious disease;
KW	organ transplant rejection; bone marrow; modulator; immune response.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Domain
FT	1..374
FT	/label= Extracellular_domain
FT	1..38
FT	/label= Leader_peptide
FT	39..442
FT	/label= Mature_human_LDCAM_polypeptide
FT	67..69
FT	/note= "N-glycosylation site"
FT	101..103
FT	/note= "N-glycosylation site"
FT	113..115
FT	/note= "N-glycosylation site"
FT	165..167
FT	/note= "N-glycosylation site"
FT	304..306
FT	/note= "N-glycosylation site"
FT	308..310
FT	/note= "N-glycosylation site"
FT	375..395
FT	/label= Transmembrane_domain
FT	396..442
FT	/label= Cytoplasmic_domain
XX	
PN	WO200008158-A2.
PD	17-FEB-2000.
XX	
PF	05-AUG-1999; 99WO-US17905.
XX	
PR	07-AUG-1998; 98US-0095672.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Baum PR, Fanslow WC;
XX	
DR	WPI: 2000-205712/18.
DR	N-PSDB: AA250862.
XX	
PT	Novel molecules designated LDCAM are capable of altering or modulating
PT	T cell function -
XX	
PS	Claim 7; Page 42-43; 4app; English.
XX	
CC	The present amino acid sequence is the human lymphoid derived dendritic
CC	cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
CC	cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
CC	region of B7-1. Human LDCAM is expressed in breast, retina, foetal
CC	liver, spleen and heart, lung, muscle, placenta, thyroid and lung
CC	carcinoma. LDCAM polypeptides interacts with T cell surface molecules
CC	to alter signalling and inhibits T cell proliferation, bind to
CC	themselves and B7-1, an LDCAM binding protein and increases natural
CC	killer (NK) cell populations. It may be used to measure the biological

CC	activity and as quality control reagents of LDCAM binding proteins.
CC	LDCAM may be used for treating disorders associated with malfunctioning
CC	of immune system, inflammation, autoimmune disorders, viral infected
CC	cells, infectious diseases and for killing tumour cells. They are also
CC	useful for prevention or reducing the effect of organ and bone marrow
CC	transplant rejection and for modulating T cell immune responses. LDCAM
CC	polypeptides may also be used as carriers for delivering agents attached
CC	to T cells or cells bearing B7L-1.
SQ	Sequence 442 AA;
Query Match	98.6%; Score 1741; DB 21; Length 442;
Best Local Similarity	98.8%; Pred. No. 5.4e-122;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
DQ	1 IPTGGONIFETDVAIVIEGEVATISCOVNKSDSVITOLNPNROTITPRDFAPLKDSRFQ 60
DB	39 IFTGGGONLFRTKDVIYIEGEVATISCOVNKSDSVIQLNPNROTIIRDRFPLKDSRFQ 98
DQ	61 ILNFSSSELKVLSTLVNSISDEGRFCOYLTPDPQESYTTITVLVPRLMIDIQDTAVE 120
DB	99 ILNFSSSELKVLSTLVNSISDEGRFYCOLYTDPPQSYYTITVLVPPRLMLIDIQDTAVE 158
DQ	121 GEIEVNCNTAASKRATTITRMFKGKKELKGSEVEWSDMTVTYSQMLAKYHKEDDGVPV 180
DB	159 GEIEVNCNTAASKRPATTIRMFKGMTLKGKSEVEWSDMYTVTSQMLAKYHKEDDGVPV 218
DQ	181 ICQVEHPAVTGLOTRLEVOYKPOVHIOMTYPILOGLTREGDAPELCCEALGKPQPMV 240
DB	219 ICQVEHPAVTGLOTRLEVOYKPOVHIOMTYPILOGLTRREGDAPELCCEALGKPQPMV 278
DQ	241 TWVRVDDEMPQHAVLSGPRLFNNLNKTNDNGTYRCEASNIYGKAHSDYMLVYDDPTTIP 300
DB	279 TWVRVDDEMPQHAVLSGPRLFNNLNKTNDNGTYRCEASNIYGKAHSDYMLVYDDPTTIP 338
DQ	301 PPTTTTTTTTTTTTTILTIIDSRSAGEBGTIGCAVDH 336
DB	339 PPTTTTTTTTTTTTTILTIIDSRSAGEBSIRAVDH 374
 RESULT 9	
AAEI19887	ID AAEI19887 standard; Protein: 442 AA.
AC	AAEI19887;
XX	18-JUN-2002 (first entry)
DT	Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
DE	Human: hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KM	liver; lung; pancreatic cancer; cell proliferative disorder; cytosolic;
KW	gene therapy.
KX	Homo sapiens.
OS	WO200214557-A1.
PN	21-FEB-2002.
PD	15-AUG-2001; 2001MO-US25690.
PF	15-AUG-2000; 2000US-225264P.
PR	(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA	Reeves RH, Yoshinori M;
PI	WPI: 2002-241913/29.
XX	Detecting cell proliferative disorder associated with tumor suppressor
PT	lung cancer (TSLC) 1 in subject, comprises contacting proliferating
PT	cell of subject with reagent detecting TSLC1 and detecting modification

PT in TSLC1 level -
 XX
 XX
 PS Disclosure; Page 49-50; 59pp; English.
 XX
 XX
 CC The invention relates to a method for detecting cell proliferative
 CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a
 CC subject. The method comprising contacting a cell component of a
 CC proliferating cell with a reagent that detects level of the cell
 CC component in the proliferating cell and determining modification in the
 CC level of the cell component in proliferating cell as compared with a
 CC healthy cell, where modification indicates disorder associated with
 CC TSLC1. The method is useful for detecting a cell proliferative disorder
 CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
 CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
 CC therapy and for treating a cell proliferative disorder such as lung
 CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
 CC carcinoma) or pancreatic cancer associated with modification of TSLC1
 CC production, where a reagent which modulates (preferably, increases) TSLC1
 CC level in the cells, is employed. The present sequence is human TSLC1.
 CC
 XX
 SQ Sequence 442 AA:

Query Match 98.6%; Score 1741; DB 23; Length 442;
 Best Local Similarity 98.8%; Pred. No. 5.4e-122;
 Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDSQNLFTKDVYIEGEVATISCOVNKSDSVIQLNPNRQTYFRDFRPLKDSRFQ 60
 DB 39 IPTGDSQNLFTKDVYIEGEVATISCOVNKSDSVIQLNPNRQTYFRDFRPLKDSRFQ 98
 QY 61 LNFSSSELKVSILTNSISDEGRFCQLYTDPPQESTYTTIVLVPPRNLMIDIOKTFAYE 120
 DB 99 LNFSSSELKVSILTNSISDEGRFCQLYTDPPQESTYTTIVLVPPRNLMIDIOKTFAYE 158
 QY 121 GEEIEVNCCTAMASKPATTTIRMFKNKELKGKSEVEKSMQYVTSQMLKVKHKEDGVPV 180
 DB 159 GEEIEVNCCTAMASKPATTTIRMFKNKELKGKSEVEKSMQYVTSQMLKVKHKEDGVPV 218
 QY 181 ICQVEHPATVGNLQTRYLEVOYKPPVHIOMTYPLQGLREGDAFELTCEAIGKPPQVMV 240
 DB 219 ICQVEHPATVGNLQTRYLEVOYKPPVHIOMTYPLQGLREGDAFELTCEAIGKPPQVMV 278
 QY 241 TWRVVDDEMPQHAVALSGPNLFINNLKKTNGTYRCEASNIYKGAHSDYMLYVDPPTTIP 300
 DB 279 TWRVVDDEMPQHAVALSGPNLFINNLKKTNGTYRCEASNIYKGAHSDYMLYVDPPTTIP 338
 QY 301 PPTTTTTTTTTTTTTLITITDSRAGEEGTICAVDH 336
 DB 339 PPTTTTTTTTTTTTTLITITDSRAGEEGTICAVDH 374

RESULT 10
 AAB25586
 ID AAB25586 standard; Protein; 364 AA.
 XX
 AC AAB25586;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 XX Protein encoded by human secreted protein gene #11.
 DE
 XX
 XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritis;
 KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
 KW anticancer; vulnary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200029435-A1.

XX
 PD 25-MAY-2000.
 XX
 XX 27-OCT-1999; 99WO-US25031.
 PF
 XX 28-OCT-1998; 98US-0105971.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX N1 J. Ruben SM, Olsen HS, Young PE, Kenny JT, Moore PA, Wei Y;
 PI Greene JM;
 PI
 DR WPI: 2000-387742/33.
 DR N-PSDB: AAA80616.
 XX
 PT Isolated nucleic acid molecules encoding human secreted proteins are
 PT used for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases -
 XX
 XX
 PS Claim 1; Figure 28A-B; 803pp; English.
 XX
 CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given
 CC in AAA80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant;
 CC anti-inflammatory; antiarthritis; antirheumatic; dermatological;
 CC antiproliferative; antiarteriosclerotic; anticancer; vulnary;
 CC antiviral; antibacterial; and antifungal activity. The proteins,
 CC polypeptides, agonists and antagonists may be used to treat prevent
 CC and/or diagnose various disease, disorders and conditions examples of
 CC which include: immune disorders e.g. Addison's disease, rheumatoid
 CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
 CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
 CC hyperproliferative disorders such as paraproteinaemias and purpura;
 CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
 CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
 CC sequences may also be used in wound healing and the treatment of
 CC infectious diseases. The human secreted protein gene #11 and protein
 CC sequences are represented in sequences AAA80616 and AAB25586. Sequences
 CC AAA80677-A80682 represent genes related to the secreted protein gene#11.
 CC
 XX
 SQ Sequence 364 AA:

Query Match 96.0%; Score 1694; DB 21; Length 364;
 Best Local Similarity 99.4%; Pred. No. 1.4e-118;
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IPTGDSQNLFTKDVYIEGEVATISCOVNKSDSVIQLNPNRQTYFRDFRPLKDSRFQ 60
 DB 39 IPTGDSQNLFTKDVYIEGEVATISCOVNKSDSVIQLNPNRQTYFRDFRPLKDSRFQ 98
 QY 61 LNFSSSELKVSILTNSISDEGRFCQLYTDPPQESTYTTIVLVPPRNLMIDIOKTFAYE 120
 DB 99 LNFSSSELKVSILTNSISDEGRFCQLYTDPPQESTYTTIVLVPPRNLMIDIOKTFAYE 158
 QY 121 GEEIEVNCCTAMASKPATTTIRMFKNKELKGKSEVEKSMQYVTSQMLKVKHKEDGVPV 180
 DB 159 GEEIEVNCCTAMASKPATTTIRMFKNKELKGKSEVEKSMQYVTSQMLKVKHKEDGVPV 218
 QY 181 ICQVEHPATVGNLQTRYLEVOYKPPVHIOMTYPLQGLREGDAFELTCEAIGKPPQVMV 240
 DB 219 ICQVEHPATVGNLQTRYLEVOYKPPVHIOMTYPLQGLREGDAFELTCEAIGKPPQVMV 278
 QY 241 TWRVVDDEMPQHAVALSGPNLFINNLKKTNGTYRCEASNIYKGAHSDYMLYVDPPTTIP 300
 DB 279 TWRVVDDEMPQHAVALSGPNLFINNLKKTNGTYRCEASNIYKGAHSDYMLYVDPPTTIP 338
 QY 301 PPTTTTTTTTTTTTTLITITDSRA 325
 DB 339 PPTTTTTTTTTTTTTLITITDSRA 363

```
RESULT 11
AAB88427
ID AAB88427 standard; Protein: 443 AA.
XX
AC AAB88427;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0200.
XX
DE Human: secretory protein; membrane protein; vaccine; gene therapy;
KM rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-0114090.
XX
PR 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0185766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isozaki T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
DR WPI: 2001-093989/11.
XX
DR N-PSDB; AAF93854.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
XX
PS Claim 1: SEQ ID 222: 609bp + CD ROM; English.
XX
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 443 AA:
XX
Query Match 90.2%; Score 1592.5; DB 22; Length 443;
Best Local Similarity 91.4%; Pred. No. 6,8e-111;
Matches 308; Conservative 5; Mismatches 23; Indels 1; Gaps 1;
```

```
OY 1 IFTGCGQNLFTADVYIEGEVATISQGVKSDSDSVIQLNPNRQTIYFDFPLKDSRFQ 60
DB 39 IFTGCGQNLFTADVYIEGEVATISQGVKSDSDSVIQLNPNRQTIYFDFPLKDSRFQ 98
```

```
OY 61 LINFSSSELKVLTVNSISDEGRYFCOLYTDPPQSYTTITVLPVPPRNIMDIQKDRIVE 120
DB 99 LINFSSSELKVLTVNSISDEGRYFCOLYTDPPQSYTTITVLPVPPRNIMDIQKDRIVE 158
OY 121 GGEIEVNCPTAMASKPATTTTRMFKNKSELKSKSEVEGSMQYVTQSOLMKVYKREDGVPV 180
DB 159 GGEIEVNCPTAMASKPATTTTRMFKNKSELKSKSEVEGSMQYVTQSOLMKVYKREDGVPV 218
OY 181 ICQVEHPAVTGNLQOTORYLEVOYKPPQVHIQMTYPLQGLTREGDAFELTCEAIGKPPVAV 240
DB 219 ICQVEHPAVTGNLQOTORYLEVOYKPPQVHIQMTYPLQGLTREGDAFELTCEAIGKPPVAV 278
OY 241 TWVRVDDDEKPOHAVALSGPMLFTNNLKNKTNDNGTYRCEASNIYGAHSQWLVYYDPPTTIP 300
DB 279 TWVRVDDDEKPOHAVALSGPMLFTNNLKNKTNDNGTYRCEASNIYGAHSQWLVYYDPPTTIP 338
OY 301 PPTTTTTTTTTTTTTTII-LTIIDSRAGEGCTIGADVH 336
DB 339 PAVHGLTQLPNSAEELDSELDSDRAGEGCTIRADVH 375
RESULT 12
AAV53028
ID AAV53028 standard; Protein: 414 AA.
XX
AC AAV53028;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
XX
DE Human: secreted protein; nutritional; cytokine; cell proliferation;
KM differentiation; immune stimulating; vaccine; suppression;
KM haematopoiesis regulation; tissue growth; actinin; inhibin;
KM chemotactic; chemokinetic; haemostatic; thrombolytic; receptor;
KM ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
KM tumour inhibition; gene therapy.
XX
XX
OS Homo sapiens.
XX
XX
PN W09957132-A1.
XX
PD 11-NOV-1999.
XX
PF 07-MAY-1999; 99WO-US09970.
XX
PR 07-MAY-1998; 98US-0084564.
PR 02-JUN-1998; 98US-0087645.
PR 22-JUL-1998; 98US-0093712.
PR 31-JUL-1998; 98US-0094935.
PR 10-AUG-1998; 98US-0095880.
PR 11-AUG-1998; 98US-0096068.
PR 06-MAY-1999; 99US-0096068.
XX
PA (GENY ) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;
PI Diblasio-Smith E, Wldom A;
DR WPI: 2000-052937/04.
DR N-PSDB; AA233346.
XX
PT New polynucleotides encoding secreted human proteins, derived from
PT adult placenta, adult retina, fetal brain, fetal
XX
XX
XX Claim 71; Page 416-417; 492pp; English.
XX
CC The present invention describes new human secreted proteins which were
CC isolated from adult placenta, adult retina, foetal brain, foetal kidney,
CC adult blood, adult brain, adult thyroid, adult bladder, adult neural
CC tissue, adult testes, and adult lymph node cDNA libraries. The human
```

CC secreted proteins, and the polynucleotides encoding them, are predicted
CC to have biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals. Suggested activities include nutritional activity, cytokine
CC and cell proliferation/differentiation activity, immune stimulating
CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
CC activity, tissue growth activity, haemostatic and thrombolytic
CC chemotactic/chemokinetic activity, anti-inflammatory activity,
CC cadherin/tumour invasion suppressor activity, and tumour inhibition
CC activity. The polynucleotides are also stated to be useful for gene
CC therapy. AA233316 to AA233373 encode human secreted proteins, and
CC AA232998 to AA233060 represent human secreted proteins, given in the
CC present invention.

XX Sequence 414 AA;

Query Match 89.0%; Score 1571; DB 21; Length 414;

Best Local Similarity 90.5%; Pred. No. 2.5e-109;

Matches 304; Conservative 1; Mismatches 3; Indels 28; Gaps 1;

QY 1 IPTGDGONLFTKDVYIEGEVATISQVVKSDSVIQLNPNKQTIYFRDPRFKKSRFQ 60
DB 39 IPRGDGONLFTKDVYIEGEVATISQVVKSDSVIQLNPNKQTIYFRDPRFKKSRFQ 98
QY 61 LNFSSSELKVSLLTVNSISDEGRFCQLYTPPQESYTTITVLVPPRNLMIDIOKDTAVE 120
DB 99 LNFSSSELKVSLLTVNSISDEGRFCQLYTPPQESYTTITVLVPPRNLMIDIOKDTAVE 158
QY 121 GEIEVENCAMASKPATTTIRFMFGNKELKGSFEVEMSDMYTTSQMLKVKHEDDGV 180
DB 159 GEIEVENCAMASKPATTTIRFMFGNKELKGSFEVEMSDMYTTSQMLKVKHEDDGV 218
QY 181 ICQVEHPATVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDAFELTCEAIKPOVMY 240
DB 219 ICQVEHPATVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDAFELTCEAIKPOVMY 278
QY 241 TWRVVDDEMPQHAVLSGPNLFINLNKKTONGTYRCEASNIIVGKAHSDYMLVYVDPPTTIP 300
DB 279 TWRVVDDEMPQHAVLSGPNLFINLNKKTONGTYRCEASNIIVGKAHSDYMLVYVDPPTTIP 331
QY 301 PPTTTTTTTTTTTTTLITITDSRAGEEGTICAVDH 336
DB 332 -----DSRAGEEGSIRAVDH 346

RESULT 13

AA25593

XX ID AAB25593 standard; Protein; 229 AA.

XX AC AAB25593;

XX DT 21-NOV-2000 (first entry)

XX DE Protein encoded by human secreted protein gene #11 clone H00DJ81.

XX XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
XX XX antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
XX XX anticancer; vulnery; antiviral; antibacterial; antifungal;
XX XX immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
XX XX multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
XX XX Crohn's disease; nephritis; hyperproliferative disorder;
XX XX cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
XX XX melanoma; lymphoma; wound healing; human.

OS Homo sapiens.

XX PN WO200029435-A1.

XX PD 25-MAY-2000.

XX PF 27-OCT-1999; 99WO-US25031.

XX XX

PR 28-OCT-1998; 98US-0105971.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;

PI Greene JM;

XX WPI; 2000-387742/33.

XX XX Isolated nucleic acid molecules encoding human secreted proteins are
XX XX used for the prevention, amelioration and treatment of autoimmune,
XX XX inflammatory, hyperproliferative and cardiovascular disorders, cancer,
XX XX wounds, and infectious diseases.

PS Claim 1; Page 685-686; 803pp; English.

CC The present invention relates to 12 secreted human proteins and the
CC nucleotide sequences encoding them. The polynucleotide sequences given
CC in AAB25593-AAB25593 encode the 12 secreted protein sequences given in
CC AAB25593-AAB25593. The human secreted proteins have various activities
CC dependent on the tissues in which they are expressed. Examples of the
CC activities of the proteins include: immunosuppressant;
CC anti-inflammatory; antiarthritic; antirheumatic; dermatological;
CC antiproliferative; antiarteriosclerotic; anticancer; vulnery;
CC antiviral; antibacterial; and antifungal activity. The proteins,
CC polypeptides, agonists and antagonists may be used to treat prevent
CC and/or diagnose various disease, disorders and conditions examples of
CC which include: immune disorders e.g. Addison's disease, rheumatoid
CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
CC hyperproliferative disorders such as paraproteinemia and purpura;
CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
CC sequences may also be used in wound healing and the treatment of
CC infectious diseases. The human secreted protein gene #11 and protein
CC sequences are represented in sequences AAB25593 and AAB25593. Sequences
CC AAB25593-AAB25593 represent genes related to the secreted protein gene#11.
XX XX

Sequence 229 AA;

Query Match 63.7%; Score 1124.5; DB 21; Length 229;

Best Local Similarity 95.1%; Pred. No. 2.8e-76;

Matches 214; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 110 MIDIOKDTAVEGEIEVENCAMASKPATTTIRFMFGNKELKGSFEVEMSDMYTTSQML 169
DB 1 MIDIOKDTAVEGEIEVENCAMASKPATTTIRFMFGNKELKGSFEVEMSDMYTTSQML 60
QY 170 KVKHEDDGVVVICQVEHPATVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDAFELTC 229
DB 61 KVKHEDDGVVVICQVEHPATVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDAFELTC 120
QY 230 EATGKPOPVMWVRVDDMPQHAVLSGPNLFINLNKKTONGTYRCEASNIIVGKAHSDYM 289
DB 121 EATGKPOPVMWVRVDDMPQHAVLSGPNLFINLNKKTONGTYRCEASNIIVGKAHSDYM 180
QY 290 LVYVDPPTTIPPTTTTTTTTTLITITDS-----PAGE 327
DB 181 LVYVDPPTTIPPTTTTTTTTTLITITDS-----PAGE 327

RESULT 14

AA278418

XX ID AAM78418 standard; Protein; 387 AA.

XX AC AAM78418;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 1080.

XX XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX XX vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

```
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001: 2001WO-US04098.
XX
XX 03-FEB-2000: 2000US-0496914.
XX 27-APR-2000: 2000US-0560875.
XX 20-JUN-2000: 2000US-0596075.
XX 19-JUL-2000: 2000US-0620325.
XX 01-SEP-2000: 2000US-0654936.
XX 15-SEP-2000: 2000US-0663561.
XX 20-OCT-2000: 2000US-0693325.
XX 30-NOV-2000: 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX N-PSDB: AAKS1551.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 20: Page 3307-3308; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 387 AA:
SQ
Query Match 35.8%; Score 631; DB 22; Length 387;
Best Local Similarity 40.9%; Pred. No. 4e-39;
Matches 124; Conservative 62; Mismatches 111; Indels 6; Gaps 3;
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```
DB 257 WNRGNSLEPERAEAVGETLTLPGLVSADNGTYTCEASNKHGHARALYLVVYDPAVVEA 316
QY 302 PRT 304
DB 317 QTS 319
RESULT 15
AAV33741
ID AAV33741 standard; Protein; 444 AA.
XX
XX AAV33741;
XX
XX 09-NOV-1999 (first entry)
XX
XX Beta-secretase.
XX
XX Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
XX Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..23
XX FT /Label= Signal_peptide
XX FT Protein 24..444
XX FT /Label= beta-secretase
XX FT Region 377..399
XX FT /note= "Putative transmembrane region"
XX
XX US5942400-A.
XX
XX 24-AUG-1999.
XX
XX 07-JUN-1996; 96US-0659984.
XX
XX 07-JUN-1996; 96US-0659984.
XX 07-JUN-1995; 95US-0480498.
XX 07-JUN-1995; 95US-0485152.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Anderson JP, Jacobson-Croak KL, Sinha S;
PI
XX
XX WPI: 1999-517417/43.
XX N-PSDB: AA206640.
XX
XX A method for detecting human beta-secretase cleavage of polypeptides
XX useful for identifying beta-secretase inhibitors
XX
XX Examples: Fig 1; 43pp; English.
XX
XX This sequence is the human beta-secretase enzyme polynucleotide.
XX Beta-secretase is capable of cleaving the beta-amyloid precursor protein
XX (APP) (AAV33742;swedish mutant APP). This enzyme is used in a method for
XX detecting human beta-secretase cleavage of polypeptides and for
XX identifying beta-secretase inhibitors. The protein has a deduced
XX molecular weight of 49 kD, although this is without glycosylation and
XX the expected molecular weight is therefore higher. Inhibition of
XX beta-secretase activity would be useful for chemical modelling of a
XX critical event in the pathology of Alzheimer's disease. Inhibitors of
XX beta-secretase would be useful for the prevention and treatment of
XX Alzheimer's disease and Down's syndrome.
XX
XX Sequence 444 AA:
SQ
Query Match 35.4%; Score 625.5; DB 20; Length 444;
Best Local Similarity 39.0%; Pred. No. 1.2e-38;
Matches 137; Conservative 66; Mismatches 121; Indels 27; Gaps 6;
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 07:35:55 ; Search time 55 Seconds
(without alignments)
95.678 Million cell updates/sec

Title: US-09-778-187B-4_COPY_21_356

Perfect score: 1765

Sequence: 1 IPTDQGNLFTKDYTVIEG.....LTIITDSKAGEGTIGAVDH 336

Scoring table: BLOSUM62

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	423	9	US-09-778-510-22
2	1765	100.0	423	9	US-09-778-187B-4
3	1741	98.6	440	9	US-09-944-413-61
4	1741	98.6	440	9	US-09-944-403-61
5	1741	98.6	440	9	US-09-944-896-61
6	1741	98.6	440	10	US-09-866-028-61
7	1741	98.6	440	10	US-09-944-449-61
8	1741	98.6	440	10	US-09-944-457-61
9	1741	98.6	440	10	US-09-944-862-61
10	1741	98.6	440	10	US-09-945-587-61
11	1741	98.6	440	10	US-09-945-015-61
12	1741	98.6	440	10	US-09-944-396-61
13	1741	98.6	440	10	US-09-944-097-61
14	1741	98.6	440	10	US-09-944-432-61
15	1741	98.6	440	10	US-09-943-762-61
16	1741	98.6	440	10	US-09-944-654-61
17	1741	98.6	440	10	US-09-943-851A-61
18	1741	98.6	440	12	US-10-052-586-34
19	1741	98.6	442	9	US-09-778-510-20

20	1741	98.6	442	9	US-09-778-187B-2	Sequence 2, Appl1
21	480.5	27.2	396	9	US-10-047-542-79	Sequence 79, Appl1
22	480.5	27.2	398	9	US-09-778-510-4	Sequence 4, Appl1
23	469.5	26.6	398	9	US-09-905-291A-84	Sequence 84, Appl1
24	469.5	26.6	398	9	US-09-778-510-6	Sequence 6, Appl1
25	469.5	26.6	398	9	US-09-778-187B-10	Sequence 10, Appl1
26	469.5	26.6	398	10	US-09-745-763-102	Sequence 102, App
27	469.5	26.6	398	10	US-09-909-320-84	Sequence 84, Appl1
28	469.5	26.6	398	10	US-09-909-088B-84	Sequence 84, Appl1
29	467.5	26.5	432	9	US-09-778-510-2	Sequence 2, Appl1
30	467.5	26.5	432	9	US-09-778-187B-8	Sequence 8, Appl1
31	220	12.5	344	9	US-09-978-295A-523	Sequence 523, App
32	220	12.5	344	9	US-09-966-546-4	Sequence 4, Appl1
33	220	12.5	344	9	US-09-966-546-6	Sequence 6, Appl1
34	220	12.5	344	9	US-09-978-697-533	Sequence 523, App
35	210	11.9	518	10	US-09-919-172-20	Sequence 20, Appl1
36	209	11.8	1256	9	US-10-047-542-90	Sequence 90, Appl1
37	208	11.8	662	9	US-10-047-542-80	Sequence 80, Appl1
38	207.5	11.8	550	10	US-09-764-853-794	Sequence 794, App
39	207	11.7	749	10	US-09-764-853-605	Sequence 605, App
40	205	11.6	1115	12	US-10-052-586-440	Sequence 440, App
41	204	11.6	734	10	US-09-756-551A-17	Sequence 17, Appl1
42	203	11.5	737	10	US-09-925-301-1133	Sequence 1133, Ap
43	197.5	11.2	350	9	US-09-808-602-71	Sequence 71, Appl1
44	193.5	11.0	582	9	US-09-736-457-334	Sequence 334, App
45	193	10.9	1395	9	US-09-808-602-67	Sequence 67, Appl1

ALIGNMENTS

RESULT 1
US-09-778-510-22
Sequence 22, Application US/09778510
Patent No. US20020164686A1
GENERAL INFORMATION: Baum, Peter
APPLICANT: Molcules Designated B7L1
TITLE OF INVENTION: 2844-US
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778, 510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-22

Query Match 100.0%; Score 1765; DB 9; Length 423;

Best Local Similarity 100.0%; Pred. No. 9.8e-108; Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	IPTDQGNLFTKDYTVIEGVAATISQVKNKSDSVQLNPNKOTYFDFRLKKSRRQ	60
DB	21	IPTDQGNLFTKDYTVIEGVAATISQVKNKSDSVQLNPNKOTYFDFRLKKSRRQ	80
QY	61	LINFSSSELKVSILTNVNSIDEGRYFCQLYTDPPQESYTTITVLVPRNLMIDIOKTAVE	120
DB	81	LINFSSSELKVSILTNVNSIDEGRYFCQLYTDPPQESYTTITVLVPRNLMIDIOKTAVE	140
QY	121	GEIEIENCTAAMSKPATYTRMFKGNKELKGSVEEWSMYYVTSQLMLKVKHKEDGVPV	180
DB	141	GEIEIENCTAAMSKPATYTRMFKGNKELKGSVEEWSMYYVTSQLMLKVKHKEDGVPV	200
QY	181	TCOVEHPATVGNLQORVLEYOVYKPOVHTOMYTPLOGLTRREGDAFELTCEALGKPPVAV	240
DB	201	TCOVEHPATVGNLQORVLEYOVYKPOVHTOMYTPLOGLTRREGDAFELTCEALGKPPVAV	260


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: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO: 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-413-61
Query Match          98.6%; Score 1741; DB 9; Length 440;
Best Local Similarity 98.8%; Pred. No. 3,7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 IPTGGGONLFTDVMYIEGEVATISGVNKSDDSVYQLNPNKQTYFFDFRPLKRSRQ 60
DB 37 IPTGGGONLFTDVMYIEGEVATISGVNKSDDSVYQLNPNKQTYFFDFRPLKRSRQ 96
QY 61 LNFSSSELKSLTVNSISDEGRYFCQLYTDPPQESYTTITLVPRNLMIDQKTAVE 120
DB 97 LNFSSSELKSLTVNSISDEGRYFCQLYTDPPQESYTTITLVPRNLMIDQKTAVE 156
QY 121 GEIEVNCYMAASKPATTTTTFKGNKELKGSVEEWSMAYVTVSOLMLKVHKEDGVPV 180
DB 157 GEIEVNCYMAASKPATTTTTFKGNKELKGSVEEWSMAYVTVSOLMLKVHKEDGVPV 216
QY 181 IGOVEHPATGNLQOTRYEVOYKPPQVHTQMTYPLQGLTREGDAPFLTCGALGKPPQVWV 240
DB 217 IGOVEHPATGNLQOTRYEVOYKPPQVHTQMTYPLQGLTREGDAPFLTCGALGKPPQVWV 276
QY 241 TWVRVDDENPQHAVALSGPNLFTNNLNKNTDNGTYRCFASNIYCAHSQVYLYVDPPTTIP 300
DB 277 TWVRVDDENPQHAVALSGPNLFTNNLNKNTDNGTYRCFASNIYCAHSQVYLYVDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTTILTIITDSRAGEEGTICAVDH 336
DB 337 PPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH 372
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RESULT 4

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: US-09-944-403-61
: Sequence 61, Application US/09944403
: Patent No. US20020165143A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Flavio, Ellen
: APPLICANT: Gottlieb, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
```

```

: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,403
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: NO. US20020165143A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: NO. US20020165143A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
```

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: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-403-61

Query Match      98.6%; Score 1741; DB 9; Length 440;
Best Local Similarity 98.8%; Pred. No. 3,7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDGONLFTKDVYIEGEVATISCOVNSKSDSVIQLNPNKOTIYFRDPRKDSRFQ 60
Db 37 IPTGDGONLFTKDVYIEGEVATISCOVNSKSDSVIQLNPNKOTIYFRDPRKDSRFQ 96
QY 61 LNFSSSELKVSLLNVSISDEGRFCOLYTPPOESYTTITVLVPPNLMIDIOKDTAVE 120
Db 97 LNFSSSELKVSLLNVSISDEGRFCOLYTPPOESYTTITVLVPPNLMIDIOKDTAVE 156
QY 121 GEIEVNCNMAKSPATTTTFMEKNGKELKKSSEVEESMDYTTYSQMLKVHKEDEGVPV 180
Db 157 GEIEVNCNMAKSPATTTTFMEKNGKELKKSSEVEESMDYTTYSQMLKVHKEDEGVPV 216
QY 181 ICQVEHPAVTGNLTQRYLEYEVQYKPOVHIOMTYPLQGLTFREGDAFELTCEAIKPOPVW 240
Db 217 ICQVEHPAVTGNLTQRYLEYEVQYKPOVHIOMTYPLQGLTFREGDAFELTCEAIKPOPVW 276
QY 241 TWVRVDEMPQAHVLSGPNLFINNLTNDGTVCESASNVGKAHSDYMLVYVDPPTTIP 300
Db 277 TWVRVDEMPQAHVLSGPNLFINNLTNDGTVCESASNVGKAHSDYMLVYVDPPTTIP 336
QY 301 PPTTTTITTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 336
Db 337 PPTTTTITTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 372

RESULT 5
US-09-944-896-61
: Sequence 61, Application US/09944896
: Patent No. US20020168715A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Baton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944, 896
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866, 028
: PRIOR FILING DATE: 2001-05-25
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: PRIOR APPLICATION NUMBER: 60/069, 334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069, 278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069, 425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069, 696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069, 694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069, 702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069, 870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069, 873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068, 017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070, 440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074, 086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074, 092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075, 945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112, 850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113, 296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146, 222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216, 021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218, 517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254, 311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
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; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-896-61

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Query Match	98.68;	Score 1741;	DB 9;	Length 440;
Best Local Similarity	98.88;	Pred. No. 3.7e-106;		
Matches 332; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0

Qy	1	IPRDCGNLFKDYVATVEGEVATISCVNKSDDSVIQLMNPQOTYFRPRLKKSFRQ	60
Db	37	IPRDCGNLFKDYVATVEGEVATISCVNKSDDSVIQLMNPQOTYFRPRLKKSFRQ	96
Qy	61	LNNSSELKSLVNTVSIIDSGRFCOLYDPPQESTTTTVLVPRLNMLDIQKTAVE	120
Db	97	LNNSSELKSLVNTVSIIDSGRFCOLYDPPQESTTTTVLVPRLNMLDIQKTAVE	156
Qy	121	GEIEVNVCTAMASKPATTIRMFKNKELKCKSEVEEWSMDYATYSQMLKVHKEDGVPV	180
Db	157	GEIEVNVCTAMASKPATTIRMFKNKELKCKSEVEEWSMDYATYSQMLKVHKEDGVPV	216
Qy	181	ICQVHNRAVNTGLOTORYLEVOXKRVUYNIOMTYRLOSGLTEBGAFELTCAISKRPORVMY	240
Db	217	ICQVHNRAVNTGLOTORYLEVOXKRVUYNIOMTYRLOSGLTEBGAFELTCAISKRPORVMY	276
Qy	241	TWVAVDEDMRQNALVSGPNLFINLNKNTDNGTJRCEASNIVGKAHSDYMLVYUDDPPTIR	300
Db	277	TWVAVDEDMRQNALVSGPNLFINLNKNTDNGTJRCEASNIVGKAHSDYMLVYUDDPPTIR	336
Qy	301	PRTTTTTTTTTTTTTTTTLITITDSAGEEGTIGAYDH	336
Db	337	PRTTTTTTTTTTTTTTTTLITITDSAGEEGTIGAYDH	372

RESULT 6
US-09-866-028-61

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: Sequence 61, Application US/09866028
: Patent No. US20020058309A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Bolstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1c1
: CURRENT APPLICATION NUMBER: US/09/866,028
: PRIORITY FILING DATE: 2001-05-25
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-866-028-61

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Query Match	98.6%;	Score 1741;	DB 10;	Length 440;
Best Local Similarity	98.8%;	Pred. No. 3.7e-106;		
Matches 332;	Conservative	1;	Mismatches 3;	Indels 0;
				Gaps 0

Qy	1	IPDDGOMLFKDYVATVEGEVATISCVONKSDSDV IOLLNPNROTIFYRQFRPLKOSRFQ	60
Db	37	IPDGGOMLFKDYVATVEGEVATISCVONKSDSDV IOLLNPNROTIFYRQFRPLKOSRFQ	96
Qy	61	LNFNSSSELKATSLTNVNSISDGRFCQLYDPPDESTTTITVLVPPNMLIDIOKDAVE	120
Db	97	LNFNSSSELKATSLTNVNSISDGRFCQLYDPPDESTTTITVLVPPNMLIDIOKDAVE	156
Qy	121	GEELIEVNCNTAMASKPATTTIRMFKNKNEIKGSEVEEWSMDYTVYSQLMLVHKHEDDGPV	180
Db	157	GEELIEVNCNTAMASKPATTTIRMFKNKNEIKGSEVEEWSMDYTVYSQLMLVHKHEDDGPV	216
Qy	181	ICQVENPRTVNTGLOTORYLEVQYKPOVNIQMTYRDLGSLTEBGDAFELTCEAIGKPOVNV	240
Db	217	ICQVENPRTVNTGLOTORYLEVQYKPOVNIQMTYRDLGSLTEBGDAFELTCEAIGKPOVNV	276
Qy	241	TWVRVDDDEMPHAYLSCPNLFINNMLKNTDNGTTRCEASNIYGAHSDYMLVYVDDPPTTIP	300
Db	277	TWVRVDDDEMPHAYLSCPNLFINNMLKNTDNGTTRCEASNIYGAHSDYMLVYVDDPPTTIP	336
Qy	301	PRTTTTTTTTTTTTTTTTIDSAGEEGTGAANDH	336
Db	337	PRTTTTTTTTTTTTTTTTIDSAGEEGTGAANDH	372

RESULT 7
US-09-944-449-61

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1 Sequence 61, Application US/09944449
2 Patent No. US20020102647A1
3 GENERAL INFORMATION:
4 APPLICANT: Baker, Kevin
5 APPLICANT: Bolstein, David
6 APPLICANT: Eaton, Dan
7 APPLICANT: Ferrara, Napoleone
8 APPLICANT: Filvaroff, Ellen
9 APPLICANT: Gerltsen, Mary
10 APPLICANT: Goddard, Audrey
11 APPLICANT: Godowski, Paul
12 APPLICANT: Grimaldi, Christopher
13 APPLICANT: Gurney, Austin
14 APPLICANT: Hillan, Kenneth
15 APPLICANT: Kljavin, Ivar
16 APPLICANT: Napier, Mary
17 APPLICANT: Roy, Margaret
18 APPLICANT: Tumas, Daniel
19 APPLICANT: Wood, William
20 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
21 FILE REFERENCE: P2548P1C1
22 CURRENT APPLICATION NUMBER: US/09/944,449
23 CURRENT FILING DATE: 2001-09-26
24 PRIOR APPLICATION NUMBER: 09/866, 028
25 PRIOR FILING DATE: 2001-05-25
26 PRIOR APPLICATION NUMBER: 60/067,411
27 PRIOR FILING DATE: December 3, 1997
28 PRIOR APPLICATION NUMBER: 60/069,334
29 PRIOR FILING DATE: December 11, 1997
30 PRIOR APPLICATION NUMBER: 60/069335
31 PRIOR FILING DATE: December 11, 1997
32 PRIOR APPLICATION NUMBER: 60/069,378
33 PRIOR FILING DATE: December 11, 1997
34 PRIOR APPLICATION NUMBER: 60/069,425
35 PRIOR FILING DATE: December 12, 1997
36 PRIOR APPLICATION NUMBER: 60/069,696
37 PRIOR FILING DATE: December 16, 1997
38 PRIOR APPLICATION NUMBER: 60/069,694
39 PRIOR FILING DATE: December 16, 1997
40 PRIOR APPLICATION NUMBER: 60/069,702
41 PRIOR FILING DATE: December 16, 1997
42 PRIOR APPLICATION NUMBER: 60/069,870
43 PRIOR FILING DATE: December 17, 1997
44 PRIOR APPLICATION NUMBER: 60/069,873
45 PRIOR FILING DATE: December 17, 1997

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? PRIOR APPLICATION NUMBER: 60/068,017
? PRIOR FILING DATE: December 18, 1997
? PRIOR APPLICATION NUMBER: 60/070,440
? PRIOR FILING DATE: January 5, 1998
? PRIOR APPLICATION NUMBER: 60/074,086
? PRIOR FILING DATE: February 9, 1998
? PRIOR APPLICATION NUMBER: 60/074,092
? PRIOR FILING DATE: February 9, 1998
? PRIOR APPLICATION NUMBER: 60/075,945
? PRIOR FILING DATE: February 25, 1998
? PRIOR APPLICATION NUMBER: 60/112,850
? PRIOR FILING DATE: December 16, 1998
? PRIOR APPLICATION NUMBER: 60/113,296
? PRIOR FILING DATE: December 22, 1998
? PRIOR APPLICATION NUMBER: 60/146,222
? PRIOR FILING DATE: July 28, 1999
? PRIOR APPLICATION NUMBER: PCT/US98/19330
? PRIOR FILING DATE: September 16, 1998
? PRIOR APPLICATION NUMBER: PCT/US98/25108
? PRIOR FILING DATE: December 1, 1998
? PRIOR APPLICATION NUMBER: 09/216,021
? PRIOR FILING DATE: December 16, 1998
? PRIOR APPLICATION NUMBER: 09/218,517
? PRIOR FILING DATE: December 22, 1998
? PRIOR APPLICATION NUMBER: 09/254,311
? PRIOR FILING DATE: March 3, 1999
? PRIOR APPLICATION NUMBER: PCT/US99/12252
? PRIOR FILING DATE: June 22, 1999
? PRIOR APPLICATION NUMBER: PCT/US99/21090
? PRIOR FILING DATE: September 15, 1999
? PRIOR APPLICATION NUMBER: PCT/US99/28409
? PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
? PRIOR APPLICATION NUMBER: PCT/US99/28313
? PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
? PRIOR APPLICATION NUMBER: PCT/US99/28301
? PRIOR FILING DATE: December 1, 1999
? PRIOR APPLICATION NUMBER: PCT/US99/30095
? PRIOR FILING DATE: December 16, 1999
? PRIOR APPLICATION NUMBER: PCT/US00/03565
? PRIOR FILING DATE: February 11, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/04414
? PRIOR FILING DATE: February 22, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/05841
? PRIOR FILING DATE: March 2, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/08439
? PRIOR FILING DATE: March 30, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/14042
? PRIOR FILING DATE: May 22, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/20710
? PRIOR FILING DATE: July 28, 2000
? PRIOR APPLICATION NUMBER: PCT/US00/32678
? PRIOR FILING DATE: December 1, 2000
? PRIOR APPLICATION NUMBER: PCT/US01/06520
? PRIOR FILING DATE: February 28, 2001
? NUMBER OF SEQ ID NOS: 120
? SEQ ID NO 61
? LENGTH: 440
? TYPE: PRT
? ORGANISM: Homo Sapien
US-09-944-449-61

Query Match      98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3,7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 IPTGGGQNLFTADVYIAGEVATISQVKNKSDSVYIQLINPNKQTYFRDFRPLKDSRFQ 60
DB 37 IPTGGGQNLFTADVYIAGEVATISQVKNKSDSVYIQLINPNKQTYFRDFRPLKDSRFQ 96
QY 61 LINFSSSELKSVLTVNSISDEGRYFCQLTDPQESYTTITVLVPPRNLMIDIKDTAVE 120
DB 97 LINFSSSELKSVLTVNSISDEGRYFCQLTDPQESYTTITVLVPPRNLMIDIKDTAVE 156
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QY 121 GEEIEVNCSTAMASKPATTTIRWFKGNKELKGSVEEMSDMYTTSQMLMKVHKEDGVVY 180
DB 157 GEEIEVNCSTAMASKPATTTIRWFKGNKELKGSVEEMSDMYTTSQMLMKVHKEDGVVY 216
QY 181 ICVEHPATVGNLQTORYLEVQYKPOVHIOMTYPLOGLREGAFELTECAIGKPPVWY 240
DB 217 ICVEHPATVGNLQTORYLEVQYKPOVHIOMTYPLOGLREGAFELTECAIGKPPVWY 276
QY 241 TWRVVDDEMPQHAVLGSPLNFNNLNKTDNGTGRCEASNTVGAHSDMYLYVDPPTTIP 300
DB 277 TWRVVDDEMPQHAVLGSPLNFNNLNKTDNGTGRCEASNTVGAHSDMYLYVDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 372

RESULT 8
US-09-944-457-61
? Sequence 61, Application US/09944457
? Patent No. US20020110859A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin
? APPLICANT: Botstein, David
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gerltsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Gurney, Austin
? APPLICANT: Hillan, Kenneth
? APPLICANT: Kijaviv, Ivar
? APPLICANT: Napier, Mary
? APPLICANT: Roy, Margaret
? APPLICANT: Tumas, Daniel
? APPLICANT: Wood, William
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P2548P1C1
? CURRENT FILING DATE: 2001-09-26
? PRIOR APPLICATION NUMBER: 09/866,028
? PRIOR FILING DATE: 2001-05-25
? PRIOR APPLICATION NUMBER: 60/067,411
? PRIOR FILING DATE: December 3, 1997
? PRIOR APPLICATION NUMBER: 60/069,334
? PRIOR FILING DATE: December 11, 1997
? PRIOR APPLICATION NUMBER: 60/069,335
? PRIOR FILING DATE: December 11, 1997
? PRIOR APPLICATION NUMBER: 60/069,278
? PRIOR FILING DATE: December 11, 1997
? PRIOR APPLICATION NUMBER: 60/069,425
? PRIOR FILING DATE: December 12, 1997
? PRIOR APPLICATION NUMBER: 60/069,696
? PRIOR FILING DATE: December 16, 1997
? PRIOR APPLICATION NUMBER: 60/069,694
? PRIOR FILING DATE: December 16, 1997
? PRIOR APPLICATION NUMBER: 60/069,702
? PRIOR FILING DATE: December 16, 1997
? PRIOR APPLICATION NUMBER: 60/069,870
? PRIOR FILING DATE: December 17, 1997
? PRIOR APPLICATION NUMBER: 60/069,873
? PRIOR FILING DATE: December 17, 1997
? PRIOR APPLICATION NUMBER: 60/068,017
? PRIOR FILING DATE: December 18, 1997
? PRIOR APPLICATION NUMBER: 60/070,440
? PRIOR FILING DATE: January 5, 1998
? PRIOR APPLICATION NUMBER: 60/074,086
? PRIOR FILING DATE: February 9, 1998
? PRIOR APPLICATION NUMBER: 60/074,092
? PRIOR FILING DATE: February 9, 1998
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: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-457-61

Query Match          98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Oy 1 IPTGGONLFTADVIVGGEVATISGVNKKSDSVIQLNPNKRTTYPRDFPLKDSRQ 60
Db 37 IPTGGONLFTADVIVGGEVATISGVNKKSDSVIQLNPNKRTTYPRDFPLKDSRQ 96
Oy 61 LNFSSSELKSLTVNVSISDEGRYFCQLYTDPQESYTTITVLPVPRNLMIDIQDTAVE 120
Db 97 LNFSSSELKSLTVNVSISDEGRYFCQLYTDPQESYTTITVLPVPRNLMIDIQDTAVE 156
Oy 121 GEIEVNTAAMSKPATYTRMFKGNKELKSKSEVEBSMSTYVTSQMLKVKHKEDGCVV 180
Db 157 GEIEVNTAAMSKPATYTRMFKGNTELKSKSEVEBSMSTYVTSQMLKVKHKEDGCVV 216
Oy 181 IGVHPAVTGNLQOTRYLEVQYKPOVNHQMTYPLQGLREGDAPELCEALGKQPPVAV 240
Db 217 IGVHPAVTGNLQOTRYLEVQYKPOVNHQMTYPLQGLREGDAPELCEALGKQPPVAV 276
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Oy 241 TWVRVDEMPQHAVUSGPNLFNNLKNKTNDNGTYRCEASIVGKASNDYMLVYDPTTIP 300
Db 277 TWVRVDEMPQHAVUSGPNLFNNLKNKTNDNGTYRCEASIVGKASNDYMLVYDPTTIP 336
Oy 301 PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 336
Db 337 PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 372

RESULT 9
US-09-944-862-61
: Sequence 61, Application US/09944862
: Patent No. US20020115145A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,862
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
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;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US200201151454member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US200201151454member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 61
;; LENGTH: 440
;; TYPE: prt
;; ORGANISM: Homo Sapien
US-09-944-862-61

Query Match 98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDSQNLFTKDVYIEGEVATISQVKNKSDSVIQLNPNKQITTFRDFRPLKDSRFQ 60
DB 37 IPTGDSQNLFTKDVYIEGEVATISQVKNKSDSVIQLNPNKQITTFRDFRPLKDSRFQ 96
QY 61 LNFSSSEKVSLSLTVNSISDEGRYFCQLYTDPPQESYTTITTVLVPNNLMIDQKTAVE 120
DB 97 LNFSSSEKVSLSLTVNSISDEGRYFCQLYTDPPQESYTTITTVLVPNNLMIDQKTAVE 156
QY 121 GGEIEVNCATAMASKPATITRMFKGNKELGKSEVEEMSDMYTTSQMLKVKHKEDDGVY 180
DB 157 GGEIEVNCATAMASKPATITRMFKGNKELGKSEVEEMSDMYTTSQMLKVKHKEDDGVY 216
QY 181 ICQVEHPAVTGNLQYQRYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIGKPPQVNV 240
DB 217 ICQVEHPAVTGNLQYQRYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIGKPPQVNV 276
QY 241 TTVRVDDDEPQAHAVLSGPNLFINNLKNTNGTYRCASNIYKKAHSDYMLYYDPPTTIP 300
DB 277 TTVRVDDDEPQAHAVLSGPNLFINNLKNTNGTYRCASNIYKKAHSDYMLYYDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 336
DB 337 PPTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDH 372

RESULT 10
US-09-945-587-61
; Sequence 61, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gottlisen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998


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: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020127643A1eember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020127643A1eember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-945-587-61

Query Match      98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 1PTGCGQCNFTADYVYIEBEVATISQGVNKSDDSVYQLNPNRQTYTFDFPLKSRQ 60
DB 37 1PTGCGQNFETDQVYIEBEVATISQGVNKSDDSVYQLNPNRQTYTFDFPLKSRQ 96

QY 61 LNFSSSELKSVLTNVSISDEGRYFCQLYTDPPOESYTTITVLVPPRLMIDIOKDTAVE 120
DB 97 LNFSSSELKSVLTNVSISDEGRYFCQLYTDPPOESYTTITVLVPPRLMIDIOKDTAVE 156

QY 121 GEEIEVNCAMASKPATITRMFKGNKELKSGSEVEMSDMYTTSQMLKVKHKEDGVPV 180
DB 157 GEEIEVNCAMASKPATITRMFKGNKELKSGSEVEMSDMYTTSQMLKVKHKEDGVPV 216

QY 181 TCOVEHPAVTGNLQOTRYLEVQKKPOVHQTQYPLQGLTRREGDAFLTEALGKPPVAV 240
DB 217 TCOVEHPAVTGNLQOTRYLEVQKKPOVHQTQYPLQGLTRREGDAFLTEALGKPPVAV 276

QY 241 TWVRVDEDEPQAVLSCPNLFTNNLKNKTNGTYRCEASNIYKASHDYMLVYVDPPTTIP 300
DB 277 TWVRVDEDEPQAVLSCPNLFTNNLKNKTNGTYRCEASNIYKASHDYMLVYVDPPTTIP 336

QY 301 PPTTTTTTTTTTTTTLITITDSRAGEECTIGAVDH 336
DB 337 PPTTTTTTTTTTTTTLITITDSRAGEECTIGAVDH 372

RESULT 11
US-09-945-015-61
: Sequence 61, Application US/09945015
: Patent No. US20020132768A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
```

```

: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerltsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tomas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/945,015
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020132768A1eember 30, 1999
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-015-61
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Query Match          98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 IPFGDCQNLFTKDYVYIEGVATISCOVNSKSDSVIQLNPNQOTTYFRDPRFKDSRFQ 60
   |||||
DB 37 IPFGDCQNLFTKDYVYIEGVATISCOVNSKSDSVIQLNPNQOTTYFRDPRFKDSRFQ 96
   |||||
QY 61 LNFSSSEKLVSLTNVSISEGRYFCQLYTPQESYTTTTLVPPRNLMIDIOKDTAVE 120
   |||||
DB 97 LNFSSSEKLVSLTNVSISEGRYFCQLYTPQESYTTTTLVPPRNLMIDIOKDTAVE 156
   |||||
QY 121 GERIEVNCAMASKPATTTTRMFNGKNEKLGKSEVEMSDMYTTSQMLKVNHEDEGVPY 180
   |||||
DB 157 GERIEVNCAMASKPATTTTRMFNGKNEKLGKSEVEMSDMYTTSQMLKVNHEDEGVPY 216
   |||||
QY 181 ICQVEHPATYGNLQOTRYLEVQYKPOVHIQMTYPLQGLTRREGDAFELTCEAIKPPQVWY 240
   |||||
DB 217 ICQVEHPATYGNLQOTRYLEVQYKPOVHIQMTYPLQGLTRREGDAFELTCEAIKPPQVWY 276
   |||||
QY 241 TWVRVDDEMPQAHVLSGPNLFINLNKKTONGTYRCEASNTVGRASHDYMLYVDPPTTIP 300
   |||||
DB 277 TWVRVDDEMPQAHVLSGPNLFINLNKKTONGTYRCEASNTVGRASHDYMLYVDPPTTIP 336
   |||||
QY 301 PPTTTTTTTTTTTTTTTTTTSDRAGEEGTICAVDH 336
   |||||
DB 337 PPTTTTTTTTTTTTTTTTTTSDRAGEEGTICAVDH 372
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RESULT 12
US-09-944-396-61
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; Sequence 61, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
```

```

; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-396-61

Query Match 98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;

Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGQNLFTKDVYIEGEVATISQVNSDDSVIQLNPNRQTYFRDPRPKDSRFQ 60
DB 37 IPTGQNLFTKDVYIEGEVATISQVNSDDSVIQLNPNRQTYFRDPRPKDSRFQ 96
QY 61 LNFSSSELKVLSTNSISDEGRYFCQLTDPQESYTTITVYVPRNLMIDOKTAVE 120
DB 97 LNFSSSELKVLSTNSISDEGRYFCQLTDPQESYTTITVYVPRNLMIDOKTAVE 156
QY 121 GEIEVNCAMASKPATITRMFKGNELGKSEVEESDMYTYSOLMLKVKHEDGVPV 180
DB 157 GEIEVNCAMASKPATITRMFKGNELGKSEVEESDMYTYSOLMLKVKHEDGVPV 216
QY 181 ICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIKQPQVWV 240
DB 217 ICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIKQPQVWV 276
QY 241 TWVRVDEHPQAVLSGPNLFTNNLKTNGTYRCASNIYGAHSDYMLYYDPPTTIP 300
DB 277 TWVRVDEHPQAVLSGPNLFTNNLKTNGTYRCASNIYGAHSDYMLYYDPPTTIP 336
QY 301 PPTTTTTTTTTTTLITTSRAGEEGTIGAVDH 336
DB 337 PPTTTTTTTTTTTLITTSRAGEEGSIRAVDH 372

RESULT 13

US-09-944-097-61
Sequence 61, Application US/09944097

Patient No. US20020133675A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: KJavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,097
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 15, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020133675A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US20020133675A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000

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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-097-61

Query Match      98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGDGONLETKDYVEGEVATISCOVNSKSDSVIQLLNPNOTIYFRDPRPKDSRFQ 60
DB 37 IPTGDGONLETKDYVEGEVATISCOVNSKSDSVIQLLNPNOTIYFRDPRPKDSRFQ 96
QY 61 LNFSSSELKVLNLNWSISDEGRYFCQLYDPPQESYTTITVLVPPRNLMIDIOKTAVE 120
DB 97 LNFSSSELKVLNLNWSISDEGRYFCQLYDPPQESYTTITVLVPPRNLMIDIOKTAVE 156
QY 121 GEEIEVNCSTAMASKPATITIMFKGNKELKCKSEVEKSDMYTYSQMLKVKHEDGVPV 180
DB 157 GEEIEVNCSTAMASKPATITIMFKGNTELKCKSEVEKSDMYTYSQMLKVKHEDGVPV 216
QY 181 ICQVHPAVTGNLQTORRYLEVOYKRPVHIOMTYPLQGLTREGDAFELTCEAIKPKOPVMY 240
DB 217 ICQVHPAVTGNLQTORRYLEVOYKRPVHIOMTYPLQGLTREGDAFELTCEAIKPKOPVMY 276
QY 241 TTVRVDEMPQHAVALSGPNLFNNLNKTDNGTYRCEASNIVGKASHDYMUYVDPPPTIP 300
DB 277 TTVRVDEMPQHAVALSGPNLFNNLNKTDNGTYRCEASNIVGKASHDYMUYVDPPPTIP 336
QY 301 PPTTTTTTTTTTTTTTTITTSRAGEEGTIGAVDH 336
DB 337 PPTTTTTTTTTTTTTTTITTSRAGEEGSIRAVDH 372

RESULT 14
US-09-944-432-61
; Sequence 61, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvarolf, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,432
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
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; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
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; ORGANISM: Homo Sapien
US-09-944-432-61
Query Match      98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGGQGNLFYTDVYIEGEVATISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRQ 60
   |||
DB 37 IPTGGQGNLFYTDVYIEGEVATISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRQ 96
   |||

QY 61 LNFSSSELKSVLTNVSIDEGRYFCQLYTPDPOESTYITVLPVRNLMIDIOKPTAVE 120
   |||
DB 97 LNFSSSELKSVLTNVSIDEGRYFCQLYTPDPOESTYITVLPVRNLMIDIOKPTAVE 156
   |||

QY 121 GGEIEVNCAMASKPATITRMFKGNELKSKSEVEEMSDMYTTSOLMLKVKHKEDGCVY 180
   |||
DB 157 GGEIEVNCAMASKPATITRMFKGNELKSKSEVEEMSDMYTTSOLMLKVKHKEDGCVY 216
   |||

QY 181 ICQVEHPAVTGNLQTRVLEVOYKKPOVHIQMTYPLQGLTREGDAFLCEALGKPOPVAV 240
   |||
DB 217 ICQVEHPAVTGNLQTRVLEVOYKKPOVHIQMTYPLQGLTREGDAFLCEALGKPOPVAV 276
   |||

QY 241 TTVRVNDEMPQAHAVLSGPNLFTNNLKTNGCYRCEASNIYGAHSDMYLYVDPPTTIP 300
   |||
DB 277 TTVRVNDEMPQAHAVLSGPNLFTNNLKTNGCYRCEASNIYGAHSDMYLYVDPPTTIP 336
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QY 301 PPTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDH 336
   |||
DB 337 PPTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDH 372
   |||

RESULT 15
US-09-943-762-61
; Sequence 61, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/943,762
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
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; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-762-61
Query Match      98.6%; Score 1741; DB 10; Length 440;
Best Local Similarity 98.8%; Pred. No. 3.7e-106;
Matches 332; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IPTGGQGNLFYTDVYIEGEVATISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRQ 60
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Db 97 LNFSSSELKVSLETNVSISEGRYFCOLYDPPOESYTTITVLVPPRNLMIDIOKDTAVE 156
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Db 157 GEEIEVNCCTAMASKPATTTIMFKGNKELKGSEVENSDMYTVTSQMLKVKHKEDDGV 216
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QY 241 TWVRVDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNIVGAHSDYMLYVYDPPTTIP 300
Db 277 TWVRVDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNIVGAHSDYMLYVYDPPTTIP 336
QY 301 PPTTTTTTTTTTTTTTILTTITDSRAGEEGTIGAVDH 336
Db 337 PPTTTTTTTTTTTTTTILTTITDSRAGEEGSIRAVDH 372

Search completed: November 20, 2002, 07:46:17
Job time : 57 secs